STIC Search Report
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STIC Database Tracking Number: 131671

TO: Ralph J Gitomer **Location: 3d65 / 3e71** **Art Unit: 1651** **Thursday, September 09, 2004** **Case Serial Number: 10/089019**	**From: Noble Jarrell** **Location: Biotech-Chem Library** **Rem 1B71** **Phone: 272-2556** **Noble.jarrell@uspto.gov**

Search Notes

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=> d his

     (FILE 'HOME' ENTERED AT 11:38:24 ON 09 SEP 2004)

     FILE 'HCAPLUS' ENTERED AT 11:39:52 ON 09 SEP 2004
                E DEWOLF W/AU
L1            57 E5-9
                E KALLENDAR H/AU
L2            35 E4-6
                E LONSDALE J/AU
L3            49 E8,E12-14
L4         11949 (SMITHKLINE OR BEECHAM OR AFFINIUM)/CS,PA
L5             7 L1-3 AND (FATTY(1A) ACID?)/TI

     FILE 'REGISTRY' ENTERED AT 11:51:40 ON 09 SEP 2004

     FILE 'HCAPLUS' ENTERED AT 11:51:47 ON 09 SEP 2004
L6              TRA L5 1- RN :       61 TERMS

     FILE 'REGISTRY' ENTERED AT 11:51:48 ON 09 SEP 2004
L7            61 SEA L6

     FILE 'WPIX' ENTERED AT 11:51:52 ON 09 SEP 2004
                E DEWOLF W/AU
L8             7 E3,E5
                E KALLENDAR H/AU
L9            24 E3-4
                E LONSDALE J/AU
L10           13 E3,E6
L11         6517 (SMITHKLINE OR BEECHAM OR AFFINIUM)/CS,PA
L12            6 L8-10 AND (FATTY (1A) ACID?)/BIX
                SEL AN 3
L13            1 E1 AND L12

     FILE 'HCAPLUS' ENTERED AT 11:55:04 ON 09 SEP 2004
L14            1 L5 AND SCREENING/TI

     FILE 'REGISTRY' ENTERED AT 11:56:32 ON 09 SEP 2004

     FILE 'HCAPLUS' ENTERED AT 11:56:39 ON 09 SEP 2004
L15             TRA L14 1- RN :       53 TERMS

     FILE 'REGISTRY' ENTERED AT 11:56:39 ON 09 SEP 2004
L16           53 SEA L15

=> b hcap
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FILE COVERS 1907 - 9 Sep 2004  VOL 141 ISS 11
FILE LAST UPDATED: 8 Sep 2004  (20040908/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

=> d all l14

L14  ANSWER 1 OF 1  HCAPLUS  COPYRIGHT 2004 ACS on STN
AN   2001:320082  HCAPLUS
DN   134:337918
ED   Entered STN:  04 May 2001
```

TI **Screening** for compds. affecting **fatty acid** biosynthesis and making **fatty acid** synthesis pathway reagents using **fatty acid** biosynthesis pathway enzymes

IN Dewolf, Walter, Jr.; **Kallender, Howard; Lonsdale, John T.**

PA Smithkline Beecham Corp., USA; Smithkline Beecham Plc

SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N009-04
ICS C12Q001-26; C12Q001-32

CC 9-2 (Biochemical Methods)
Section cross-reference(s): 1, 7, 22

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001030988	A1	20010503	WO 2000-US29451	20001026

W: JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRAI US 1999-161775P P 19991027

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2001030988	ICM	C12N009-04
	ICS	C12Q001-26; C12Q001-32

AB Provided is a screening method for compds. affecting fatty acid biosynthesis, the method comprising: (A) providing a reaction mixture comprising: (1) (a) an acyl carrier moiety or (b) enzymes and precursors sufficient to generate the acyl carrier moiety; (2) a bacterial enzymic pathway comprising at least two (preferably three, four or five) consecutively acting enzymes selected from the group consisting of: (a) malonyl-CoA:ACP transacylase, (b) .beta.-ketoacyl-ACP synthase III, (c) NADPH-dependent .beta.-ketoacyl-ACP reductase, (d) .beta.-hydroxyacyl-ACP dehydrase, and (e) enoyl-ACP reductase; and (3) substrates and cofactors required for the operation of the enzymes; (B) contacting the reaction mixture with a prospective bioactive agent; (C) conducting a high throughput measurement of the activity of the enzymic pathway; and (D) determining if the contacting altered the activity of the enzymic pathway. Further provided is a screening method for compds. affecting fatty acid biosynthesis: (A) providing a reaction mixture comprising: (1) (a) an acyl carrier moiety or (b) enzymes and precursors sufficient to generate the acyl carrier moiety; (2) a bacterial enzymic pathway comprising at least two consecutively acting enzymes selected from: (a) malonyl-CoA:ACP transacylase, (b) .beta.-ketoacyl-ACP synthase III, (c) NADPH-dependent .beta.-ketoacyl-ACP reductase, (d) .beta.-hydroxyacyl-ACP dehydrase, and (e) enoyl-ACP reductase; and (3) substrates and cofactors required for the operation of the enzymes; (B) contacting the reaction mixture with a prospective bioactive agent; (C) measuring the activity of the enzymic pathway; and (D) determining if the contacting altered the activity of the enzymic pathway, wherein at least one of the following applies: (1) the enoyl-ACP reductase is a NADH-specific enoyl-ACP reductase; or (2) the .beta.-ketoacyl-ACP synthase III is a .beta.-ketoacyl-ACP synthase III derived from E.coli. or H. influenzae; or (3) NADPH is provided to the reacting step in a constant amount such that the NADH consumption by enoyl-ACP reductase (FabI) can be quantitated accurately and without interference, or an amount effective to reduce NADH consumption by more NADPH-dependent enzymes; or (4) the NADPH-dependent .beta.-ketoacyl-ACP reductase is derived from Streptococcus, Staphylococcus or Pseudomonas.

ST fatty acid biosynthesis pathway screening enzyme; ACP fatty acid pathway enzyme Streptococcus Staphylococcus Pseudomonas

IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(ACP (acyl-carrier), acyl-; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT Proteins, specific or class
RL: ARG (Analytical reagent use); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
(ACP (acyl-carrier); screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT Drug screening

Escherichia
Escherichia coli
Haemophilus influenzae
Metabolic pathways
Pseudomonas
Staphylococcus
Staphylococcus aureus
Streptococcus
Streptococcus pneumoniae
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT Fatty acids, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 56-45-1, L-Serine, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(-37, of ACP; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 9077-10-5, .beta.-Ketoacyl-ACP synthetase
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); CAT (Catalyst use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(III; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 37250-34-3, .beta.-Ketoacyl-ACP reductase
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); CAT (Catalyst use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(NADPH-dependent; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 53-57-6, NADPH 58-68-4, NADH 35840-73-4
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 37237-39-1, .beta.-Hydroxyacyl-ACP dehydrase 37251-08-4, Enoyl-ACP reductase 37257-17-3, Malonyl-CoA transacylase
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); CAT (Catalyst use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 337526-90-6DP, complex with acyl carrier protein 337526-92-8DP, complex with acyl carrier protein 337526-94-0DP, complex with acyl carrier protein 337526-96-2DP, complex with acyl carrier protein 337526-97-3DP, complex with acyl carrier protein 337526-99-5P 337527-00-1P
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 140345-60-4, DNA (Escherichia coli clone pWO114 gene fabH plus flanks) 329083-57-0 206887-32-3, DNA (Streptococcus pneumoniae gene fabH) 338475-24-4, 1: PN: WO0130988 SEQID:17 unclaimed DNA 338475-26-6, 4: PN: WO0130988 SEQID: 19 unclaimed DNA 338475-27-7, 8: PN: WO0130988 SEQID: 23 unclaimed DNA 338475-28-8 338475-30-2 338475-31-3 338475-33-5 338475-35-7 338475-36-8 338475-37-9 338475-39-1, 23: PN: WO0130988 SEQID: 1 unclaimed DNA 338475-42-6, 26: PN: WO0130988 SEQID: 4 unclaimed DNA 338475-45-9, 29: PN: WO0130988 SEQID: 7 unclaimed DNA 338475-47-1, 31: PN: WO0130988 SEQID: 9 unclaimed DNA 338475-49-3
RL: PRP (Properties)
(unclaimed nucleotide sequence; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 146890-02-0, Protein ACP (Escherichia coli clone pMR24 gene acpP acyl-carrier) 146890-24-6 148998-18-9, Protein (Escherichia coli clone

pHAP1 gene envM reduced) 200143-22-2 206887-31-2 315726-50-2
329083-56-9 338475-25-5 338475-29-9 338475-32-4 338475-34-6
338475-38-0 338475-40-4 338475-41-5 338475-43-7 338475-44-8
338475-46-0 338475-48-2 338475-50-6
RL: PRP (Properties)
(unclaimed protein sequence; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Dick; US 5614551 A 1997 HCAPLUS
(2) Kuhajda; US 5759837 A 1998 HCAPLUS
(3) Roujeinkova, A; Journal of Biological Chemistry 1999, V274(43), P30811
(4) Royer; US 5539132 A 1996 HCAPLUS
(5) Ward, W; Biochemistry V38(38), P12514 HCAPLUS

=> b wpix
FILE 'WPIX' ENTERED AT 11:57:30 ON 09 SEP 2004
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FILE LAST UPDATED: 7 SEP 2004 <20040907/UP>
MOST RECENT DERWENT UPDATE: 200457 <200457/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

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>>> NEW DISPLAY FORMAT HITSTR ADDED ALLOWING DISPLAY OF HIT STRUCTURES WITHIN THE BIBLIOGRAPHIC DOCUMENT <<<

=> d all l13

L13 ANSWER 1 OF 1 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **2001-316332** [33] WPIX
DNC C2001-097452
TI High throughput method for screening for biological agents against **fatty acid** biosynthesis comprises contacting a bacterial enzymatic pathway with enzymes e.g. malonyl-CoA ACP transacylase.
DC B04 D16
IN **DEWOLF, W**; **KALLENDER, H**; **LONSDALE, J T**
PA (SMIK) SMITHKLINE BEECHAM CORP; (SMIK) SMITHKLINE BEECHAM PLC
CYC 20
PI WO 2001030988 A1 20010503 (200133)* EN 94 C12N009-04
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: JP US
ADT WO 2001030988 A1 WO 2000-US29451 20001026
PRAI US 1999-161775P 19991027
IC ICM C12N009-04
ICS C12Q001-26; C12Q001-32
AB WO 200130988 A UPAB: 20010615
NOVELTY - A high throughput method for screening for biological agents affecting **fatty acid** biosynthesis, comprises contacting a bacterial enzymatic pathway with enzymes.
DETAILED DESCRIPTION - A high throughput screening method for biological agents affecting **fatty acid** biosynthesis, comprises:
(a) providing a mixture containing an acyl carrier protein (ACP) or functional group or the enzymes and precursors sufficient to generate the acyl carrier group, a bacterial enzymatic pathway comprising at least two consecutively acting enzymes selected from malonyl-CoA:ACP transacylase, beta -ketoacyl-ACP synthase III, NADPH-dependent beta -ketoacyl-ACP reductase, beta -hydroxyacyl-ACP dehydrase, and enoyl-ACP reductase, and

first substrates and cofactors required for the operation of the enzymes;
(b) contacting the reaction mixtures;
(c) conducting a high throughput measurement of the activity of the enzymatic pathway; and
(d) determining if the contacting altered the activity of the enzymatic pathway.
An INDEPENDENT CLAIM is also included for a method for attachment of a phosphopantetheinyl prosthetic group to apo-AC, comprising providing apo-ACP and chemically adding a phosphopantetheinyl prosthetic group.
USE - The method is used for screening for biological agents affecting **fatty acid** biosynthesis.
Dwg.0/3
FS CPI
FA AB; DCN
MC CPI: B04-B01B; B04-E03E; B04-E03F; B04-E08; B04-F10; B04-L03D; B04-L06; B04-N02; B11-C08E3; B12-K04A; D05-A02A; D05-A02D; D05-H09

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STRUCTURE FILE UPDATES:    8 SEP 2004  HIGHEST RN 741635-85-8
DICTIONARY FILE UPDATES:   8 SEP 2004  HIGHEST RN 741635-85-8

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

  Please note that search-term pricing does apply when
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Crossover limits have been increased.  See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
http://www.cas.org/ONLINE/DBSS/registryss.html

=> d ide l34 tot

L34  ANSWER 1 OF 5  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   37257-17-3  REGISTRY
CN   Malonyltransferase, [acyl carrier protein] (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   E.C. 2.3.1.39
CN   Malonyl CoA-ACP transacylase
CN   Malonyl CoA:ACP acyltransferase
CN   Malonyl coenzyme A-acyl carrier protein transacylase
CN   Malonyl transacylase
CN   Malonyl transferase
CN   Malonyl-CoA transacylase
CN   Malonyl-CoA-acyl carrier protein transacylase
CN   Malonyl-CoA:acyl carrier protein S-acyltransferase
CN   [Acyl carrier protein]malonyltransferase
DR   37278-91-4
MF   Unspecified
CI   MAN
LC   STN Files:   AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CASREACT,
       TOXCENTER, USPAT2, USPATFULL
DT.CA  CAplus document type:  Conference; Dissertation; Journal; Patent
RL.P   Roles from patents:  ANST (Analytical study); BIOL (Biological study);
       OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties);
       USES (Uses)
RL.NP  Roles from non-patents:  ANST (Analytical study); BIOL (Biological
       study); FORM (Formation, nonpreparative); MSC (Miscellaneous); OCCU
       (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); USES
       (Uses); NORL (No role in record)
RLD.NP Roles for non-specific derivatives from non-patents:  BIOL (Biological
       study); PRP (Properties)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
             173 REFERENCES IN FILE CA (1907 TO DATE)
               1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
             173 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L34  ANSWER 2 OF 5  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   37251-08-4  REGISTRY
CN   Reductase, enoyl-[acyl carrier protein] (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   E.C. 1.3.1.9
CN   Enoyl-ACP reductase
CN   Enoyl-[acyl carrier protein] reductase
CN   NADH-dependent enoyl acyl carrier protein reductase
CN   NADH-enoyl acyl carrier protein reductase
CN   NADH-enoyl-ACP reductase
CN   NADH-specific enoyl-ACP reductase
MF   Unspecified
CI   MAN
LC   STN Files:   AGRICOLA, ANABSTR, BIOSIS, CA, CAPLUS, CEN, TOXCENTER,
       USPAT2, USPATFULL
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DT.CA CAplus document type: Conference; Dissertation; Journal; Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); MSC (Miscellaneous); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); USES (Uses)
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RL.NP Roles from non-patents: ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); MSC (Miscellaneous); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); RACT (Reactant or reagent); USES (Uses); NORL (No role in record)
RLD.NP Roles for non-specific derivatives from non-patents: BIOL (Biological study); PROC (Process); PRP (Properties)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
224 REFERENCES IN FILE CA (1907 TO DATE)
13 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
226 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L34 ANSWER 3 OF 5 REGISTRY COPYRIGHT 2004 ACS on STN
RN **37250-34-3** REGISTRY
CN Reductase, 3-oxoacyl- [acyl carrier protein] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN .beta.-Ketoacyl reductase
CN .beta.-Ketoacyl thioester reductase
CN .beta.-Ketoacyl-ACP reductase
CN .beta.-Ketoacyl-acyl carrier protein reductase
CN 3-Ketoacyl acyl carrier protein reductase
CN 3-Oxoacyl-[ACP]-reductase
CN 3-Oxoacyl-[acyl carrier protein] reductase
CN E.C. 1.1.1.100
CN NADPH-specific 3-oxoacyl-[acylcarrier protein]reductase
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, ANABSTR, BIOSIS, CA, CAPLUS, CASREACT, CEN, TOXCENTER, USPATFULL
DT.CA CAplus document type: Conference; Dissertation; Journal; Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); USES (Uses)
RLD.P Roles for non-specific derivatives from patents: BIOL (Biological study)
RL.NP Roles from non-patents: ANST (Analytical study); BIOL (Biological study); MSC (Miscellaneous); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); RACT (Reactant or reagent); USES (Uses); NORL (No role in record)
RLD.NP Roles for non-specific derivatives from non-patents: BIOL (Biological study); PRP (Properties)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
183 REFERENCES IN FILE CA (1907 TO DATE)
5 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
183 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L34 ANSWER 4 OF 5 REGISTRY COPYRIGHT 2004 ACS on STN
RN **37237-39-1** REGISTRY
CN Dehydratase, 3-hydroxyacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN .beta.-Hydroxyacyl-ACP dehydrase
CN .beta.-Hydroxyacyl-[ACP] dehydratase
CN 3-Hydroxyacyl-ACP dehydratase
CN 3-Hydroxyacyl-[acyl carrier protein] dehydratase
MF Unspecified
CI MAN
LC STN Files: BIOSIS, CA, CAPLUS, TOXCENTER, USPATFULL
DT.CA CAplus document type: Dissertation; Journal; Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); PREP (Preparation); PRP (Properties); USES (Uses)
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22 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L34 ANSWER 5 OF 5 REGISTRY COPYRIGHT 2004 ACS on STN

RN **9077-10-5** REGISTRY
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN .beta.-Ketoacyl synthetase
CN .beta.-Ketoacyl-ACP synthase
CN .beta.-Ketoacyl-ACP synthetase
CN .beta.-Ketoacyl-acyl carrier protein synthetase
CN .beta.-Ketoacyl-[acyl carrier protein] synthase
CN .beta.-Ketoacylsynthase
CN 3-Ketoacyl acyl carrier protein synthetase
CN 3-Ketoacyl-ACP synthase
CN 3-Ketoacyl-acyl carrier protein synthase
CN 3-Ketoacyl-[ACP]-synthetase
CN 3-Oxoacyl-ACP synthase
CN 3-Oxoacyl-[acyl carrier protein] synthase
CN Condensing enzyme
CN E.C. 2.3.1.41
CN Fatty acid condensing enzyme
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CEN, CIN, EMBASE, PROMT, TOXCENTER, USPAT2, USPATFULL
DT.CA CAplus document type: Conference; Dissertation; Journal; Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); MSC (Miscellaneous); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); USES (Uses)
RLD.P Roles for non-specific derivatives from patents: BIOL (Biological study); PREP (Preparation); PRP (Properties); USES (Uses)
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*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
431 REFERENCES IN FILE CA (1907 TO DATE)
7 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
432 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> d his

(FILE 'HOME' ENTERED AT 11:38:24 ON 09 SEP 2004)

FILE 'HCAPLUS' ENTERED AT 11:39:52 ON 09 SEP 2004
E DEWOLF W/AU
L1 57 E5-9
E KALLENDAR H/AU
L2 35 E4-6
E LONSDALE J/AU
L3 49 E8,E12-14
L4 11949 (SMITHKLINE OR BEECHAM OR AFFINIUM)/CS,PA

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L5 7 L1-3 AND (FATTY(1A) ACID?)/TI

FILE 'REGISTRY' ENTERED AT 11:51:40 ON 09 SEP 2004

FILE 'HCAPLUS' ENTERED AT 11:51:47 ON 09 SEP 2004
L6 TRA L5 1- RN : 61 TERMS

FILE 'REGISTRY' ENTERED AT 11:51:48 ON 09 SEP 2004
L7 61 SEA L6

FILE 'WPIX' ENTERED AT 11:51:52 ON 09 SEP 2004
E DEWOLF W/AU
L8 7 E3,E5
E KALLENDAR H/AU
L9 24 E3-4
E LONSDALE J/AU
L10 6517 (SMITHKLINE OR BEECHAM OR AFFINIUM)/CS,PA
L11 6 L8-L*** AND (FATTY (1A) ACID?)/BIX

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                SEL AN 3
L12           1 E1 AND L11

     FILE 'HCAPLUS' ENTERED AT 11:55:04 ON 09 SEP 2004
L13           1 L5 AND SCREENING/TI

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     FILE 'HCAPLUS' ENTERED AT 11:56:39 ON 09 SEP 2004
L14           TRA L13 1- RN :       53 TERMS

     FILE 'REGISTRY' ENTERED AT 11:56:39 ON 09 SEP 2004
L15          53 SEA L14

     FILE 'HCAPLUS' ENTERED AT 12:25:00 ON 09 SEP 2004
                E HIGH THROUGHPUT SCREENING/CT
                E E3+ALL
L16         3861 HIGH THROUGHPUT SCREENING/CT
                E HTS/CT
                E HIGH SPEED/CT
                E E5+ALL
                E DRUG SCREENING/CT
                E E3+ALL
L17        31006 DRUG SCREENING+OLD/CT
                E DRUG DESIGN/CT
                E E3+ALL
                E DRUG DISCOVERY/CT
                E E3+ALL
                E COMBINATORIAL LIBRARY/CT
                E E3+ALL
L18         9375 COMBINATORIAL LIBRARY+NT/CT
                E E7+ALL
L19         5485 NUCLEIC ACID LIBRARY+NT/CT
                E NUCLEIC ACID/CT
                E E22+ALL
                E E11+ALL
L20        32478 NUCLEIC ACID HYBRIDIZATION+OLD,NT/CT
                E E4+AL
                E E3+ALL
L21        17876 MICROARRAY TECHNOLOGY+NT/CT
                E ANALYTICAL APPARATUS/CT
                E E3+ALL
L22         8751 ANALYTICAL APPARATUS+NT/CT
                E ANALYSIS/CT
L23        30185 ANALYSIS/CW (L) APP?
                E BIOTECHNOLOGY/CT
                E E3+ALL
L24         1104 BIOTECHNOLOGY/CT (L) BIOCHIP?
                E TECHNOLOGY/CT
                E E3+ALL
L25         6690 TECHNOLOGY+OLD,NT/CT (L) BIO?

     FILE 'REGISTRY' ENTERED AT 12:37:15 ON 09 SEP 2004
L26           1 9077-10-5
L27           1 37250-34-3
L28           1 37237-39-1
L29           1 37251-08-4
L30           1 37257-17-3
L31        2827 ACYL (1A) CARRIER
L32           5 L26-30

     FILE 'HCAPLUS' ENTERED AT 12:46:30 O
L33         813 L32
L34         130 MALONYL (1A) ((COENZYME O                                    YLTRANS
L35         206 (NADH (1A) ENOYL OR ENOYL)                                   R (1A)
L36         165 BETA (1A) KETOACYL (3A) RE                                   L) (1A)
L37           4 BETA (1A) HYDROXYACYL (1A)                                   IN OR A
L38         415 (BETA (1A) KETOACYL OR KETOACYL OR OXOACYL) (2A) (ACYL(1A) CARR

     FILE 'REGISTRY' ENTERED AT 13:00:37 ON 09 SEP 2004
L39        2821 L31 AND MAN/CI

     FILE 'HCAPLUS' ENTERED AT 13:01:03 ON 09 SEP 2004
L40        1738 L39
                E COFACTOR/CT
                E COFACTORS/CT
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L37: 1-34 in previous page

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                E COENZYME/CT
                E COENZYME/CT
                E COENZYMES/CT
                E E3+ALL
L41         19134 COENZYMES+NT/CT
L42             4 (ACYLCARRIER (1A) PROTEIN) (3A) (NADH (1A) ENOYL OR ENOYL OR BE
L43           831 L40 AND (L33 OR L34 OR L35 OR L36 OR L37 OR L38 OR L42)
L44            88 L43 AND L41
L45            65 L44 AND (PY<=1999 OR AY<=1999 OR PRY<=1999 OR PD<19991027 OR AD
                E FATTY ACID/CT
                E FATTY ACID/CT
                E BIOSYNTHESIS/CT
                E E3+ALL
                E FATTY ACIDS/CT
                E E3+ALL
L46        342292 FATTY ACIDS+NT/CT
                E E179
                E E3+ALL
L47          5793 L46 (L) (PATHWAY? OR BIOSYNTHES? OR SYNTHES?)
                E "FATTY ACIDS, BIOLOGICAL"/CT
L48        101605 ("FATTY ACIDS, BIOLOGICAL STUDIES" OR "FATTY ACIDS, FORMATION (
L49            19 L45 AND L47-48
L50         45512 SCREEN?/CW
                E LAB/CT
                E E6
                E E6+ALL
                E LAB/CT
                E E6+ALL
                E E3+ALL
L51         19537 LAB-ON-A-CHIP+NT/CT
L52             0 L45 AND (L50 OR L51 OR L16 OR L17 OR L18 OR L19 OR L19 OR L20 O
L53           385 L47-48 AND (L50 OR L51 OR L16 OR L17 OR L18 OR L19 OR L19 OR L***
L54             9 L53 AND (L33 OR L34 OR L35 OR L36 OR L37 OR L38 OR L42)
L55            17 L53 AND L40
L56             6 L54 AND (PY<=1999 OR PRY<=1999 OR AY<=1999 OR PD<19991027 OR AD
L57            11 L55 AND (PY<=1999 OR PRY<=1999 OR AY<=1999 OR PD<19991027 OR AD
L58             2 L1-3 AND L54-55
L59             9 L56-57 NOT L58
                SEL AN 1 3 8
L60             6 L59 NOT E1-6
                E LIPID BIOSYNTH/CT
                E E14+ALL
                E LIPIDS/CT
L61        151285 LIPID?/CW
L62          1585 L61 (L)(PATHWAY? OR BIOSYNTHES? OR SYNTHES?)
L63            60 (L16 OR L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23 OR L24 OR
L64             4 (L33 OR L34 OR L35 OR L36 OR L38 OR L40 OR L42) AND L63
L65             0 L64 AND L1-4
L66             1 L64 AND (PY<=1999 OR AY<=1999 OR PRY<=1999 OR AD<19991027 OR PR
L67             6 L60 OR L66
L68           181 L41 AND (L33 OR L34 OR L35 OR L36 OR L38 OR L40 OR L42)
L69             3 L68 AND (L16 OR L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23 O
L70             0 L69 AND L1-4
L71             0 L69 AND (PY<=1999 OR AY<=1999 OR PRY<=1999 OR AD<19991027 OR PD
L72            44 L68 AND (L47 OR L48 OR L62)
L73            36 L72 AND (PY<=1999 OR AY<=1999 OR PRY<=1999 OR AD<19991027 OR PD
L74             3 L73 AND P/DT
L75             2 L72 AND L1-4
L76            42 L72 NOT L75
L77            35 L76 AND (PY<=1999 OR AY<=1999 OR PRY<=1999 OR AD<19991027 OR PD
L78             2 L77 AND P/DT
L79             1 CORYNEBACTERIUM AND L78
L80            33 L77 NOT L78

     FILE 'HCAPLUS' ENTERED AT 15:06:22 ON 09 SEP 2004
                SEL AN 3-6
L81             4 E1-8 AND L80
L82            29 L80 NOT L81
                SEL AN 25 20 17 19
L83            25 L82 NOT E9-16
L84            26 L79 OR L83
L85             4 L75 OR L58

=> b hcap
FILE 'HCAPLUS' ENTERED AT 15:23:05 ON 09 SEP 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE COVERS 1907 - 9 Sep 2004 VOL 141 ISS 11
FILE LAST UPDATED: 8 Sep 2004 (20040908/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

=> d all l85 tot

L85 ANSWER 1 OF 4 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:613222 HCAPLUS
DN 136:212642
ED Entered STN: 23 Aug 2001
TI Identification, substrate specificity, and inhibition of the Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH)
AU Khandekar, Sanjay S.; Gentry, Daniel R.; Van Aller, Glenn S.; Warren, Patrick; Xiang, Hong; Silverman, Carol; Doyle, Michael L.; Chambers, Pamela A.; Konstantinidis, Alex K.; Brandt, Martin; Daines, Robert A.; **Lonsdale, John T.**
CS Department of Protein Biochemistry, Glaxo **SmithKline**, King of Prussia, PA, 19406, USA
SO Journal of Biological Chemistry (2001), 276(32), 30024-30030
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
CC 7-3 (Enzymes)
Section cross-reference(s): 3, 10
AB In the bacterial type II fatty acid synthase system, .beta.-ketoacyl-acyl carrier protein (ACP) synthase III (FabH) catalyzes the condensation of acetyl-CoA with malonyl-ACP. We have identified, expressed, and characterized the Streptococcus pneumoniae homolog of Escherichia coli FabH. S. pneumoniae FabH is .apprx.41, 39, and 38% identical in amino acid sequence to Bacillus subtilis, E. coli, and Hemophilus influenzae FabH, resp. The His-Asn-Cys catalytic triad present in other FabH mols. is conserved in S. pneumoniae FabH. The apparent Km values for acetyl-CoA and malonyl-ACP were determined to be 40.3 and 18.6 .mu.M, resp. Purified S. pneumoniae FabH preferentially utilized straight short-chain CoA primers. Similar to E. coli FabH, S. pneumoniae FabH was weakly inhibited by thiolactomycin. In contrast, inhibition of S. pneumoniae FabH by the newly developed compound SB418011 was very potent, with an IC50 value of 0.016 .mu.M. SB418011 also inhibited E. coli and H. influenzae FabH with IC50 values of 1.2 and 0.59 .mu.M, resp. The availability of purified and characterized S. pneumoniae FabH will greatly aid in structural studies of this class of essential bacterial enzymes and facilitate the identification of small mol. inhibitors of type II fatty acid synthase with the potential to be novel and potent antibacterial agents active against pathogenic bacteria.
ST Streptococcus **ketoacyl acyl carrier protein synthase** FabH; gene sequence Streptococcus FabH **ketoacyl acyl carrier protein synthase**
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ACP (acyl-carrier), S-malonyl, substrate; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))
IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(FabH; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(esters, with CoA, substrates; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT DNA sequences
Michaelis constant
Protein sequences
Streptococcus pneumoniae
(identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT **9077-10-5P**
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)
(III, gene FabH; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT **402819-83-4P**
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)
(amino acid sequence; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT 82079-32-1, Thiolactomycin 313963-95-0, SB 418011
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inhibitor; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT **385255-20-9**, GenBank AF384041
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT 2140-48-9, Butyryl-CoA 6244-91-3, Isovaleryl-CoA 15621-60-0, Isobutyryl-CoA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(substrate; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT **72-89-9**, Acetyl-CoA
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(substrate; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

IT **85-61-0D**, Coenzyme A, fatty acid esters
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(substrates; identification, substrate specificity, and inhibition of Streptococcus pneumoniae **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH))

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

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(34) Vance, D; Biochem Biophys Res Commun 1972, V48, P649 HCAPLUS
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(36) Woody, R; Methods Enzymol 1995, V246, P34 HCAPLUS

L85 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:320082 HCAPLUS
DN 134:337918
ED Entered STN: 04 May 2001
TI Screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes
IN Dewolf, Walter, Jr.; **Kallender, Howard**; **Lonsdale, John T.**
PA Smithkline Beecham Corp., USA; Smithkline Beecham Plc
SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N009-04
ICS C12Q001-26; C12Q001-32
CC 9-2 (Biochemical Methods)
Section cross-reference(s): 1, 7, 22
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001030988	A1	20010503	WO 2000-US29451	20001026
	W: JP, US				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
PRAI	US 1999-161775P	P	19991027		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2001030988	ICM	C12N009-04
	ICS	C12Q001-26; C12Q001-32

AB Provided is a screening method for compds. affecting fatty acid biosynthesis, the method comprising: (A) providing a reaction mixture comprising: (1) (a) an acyl carrier moiety or (b) enzymes and precursors sufficient to generate the acyl carrier moiety; (2) a bacterial enzymic pathway comprising at least two (preferably three, four or five) consecutively acting enzymes selected from the group consisting of: (a) malonyl-CoA:ACP transacylase, (b) .beta.-ketoacyl-ACP synthase III, (c) NADPH-dependent .beta.-ketoacyl-ACP reductase, (d) .beta.-hydroxyacyl-ACP dehydrase, and (e) enoyl-ACP reductase; and (3) substrates and cofactors required for the operation of the enzymes; (B) contacting the reaction mixture with a prospective bioactive agent; (C) conducting a high throughput measurement of the activity of the enzymic pathway; and (D) determining if the contacting altered the activity of the enzymic pathway. Further provided

is a screening method for compds. affecting fatty acid biosynthesis: (A) providing a reaction mixture comprising: (1) (a) an acyl carrier moiety or (b) enzymes and precursors sufficient to generate the acyl carrier moiety; (2) a bacterial enzymic pathway comprising at least two consecutively acting enzymes selected from: (a) malonyl-CoA:ACP transacylase, (b) .beta.-ketoacyl-ACP synthase III, (c) NADPH-dependent .beta.-ketoacyl-ACP reductase, (d) .beta.-hydroxyacyl-ACP dehydrase, and (e) enoyl-ACP reductase; and (3) substrates and cofactors required for the operation of the enzymes; (B) contacting the reaction mixture with a prospective bioactive agent; (C) measuring the activity of the enzymic pathway; and (D) determining if the contacting altered the activity of the enzymic pathway, wherein at least one of the following applies: (1) the enoyl-ACP reductase is a NADH-specific enoyl-ACP reductase; or (2) the .beta.-ketoacyl-ACP synthase III is a .beta.-ketoacyl-ACP synthase III derived from E.coli. or H. influenzae; or (3) NADPH is provided to the reacting step in a constant amount such that the NADH consumption by enoyl-ACP reductase (FabI) can be quantitated accurately and without interference, or an amount effective to reduce NADH consumption by more NADPH-dependent enzymes; or (4) the NADPH-dependent .beta.-ketoacyl-ACP reductase is derived from Streptococcus, Staphylococcus or Pseudomonas.

ST fatty acid biosynthesis pathway screening enzyme; ACP fatty acid pathway enzyme Streptococcus Staphylococcus Pseudomonas

IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(ACP (acyl-carrier), acyl-; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT Proteins, specific or class
RL: ARG (Analytical reagent use); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
(ACP (acyl-carrier); screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT **Drug screening**
Escherichia
Escherichia coli
Haemophilus influenzae
Metabolic pathways
Pseudomonas
Staphylococcus
Staphylococcus aureus
Streptococcus
Streptococcus pneumoniae
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(screening for compds. affecting fatty acid **biosynthesis** and making fatty acid **synthesis pathway** reagents using fatty acid **biosynthesis pathway** enzymes)

IT 56-45-1, L-Serine, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(-37, of ACP; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT **9077-10-5, .beta.-Ketoacyl-ACP synthetase**
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); CAT (Catalyst use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(III; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT **37250-34-3, .beta.-Ketoacyl-ACP reductase**
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); CAT (Catalyst use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(NADPH-dependent; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 53-57-6, NADPH 58-68-4, NADH 35840-73-4

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT **37237-39-1**, .beta.-Hydroxyacyl-ACP dehydrase **37251-08-4**, **Enoyl-ACP reductase 37257-17-3**, **Malonyl-CoA transacylase**
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); CAT (Catalyst use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT **337526-90-6DP**, complex with acyl carrier protein
337526-92-8DP, complex with acyl carrier protein
337526-94-0DP, complex with acyl carrier protein
337526-96-2DP, complex with acyl carrier protein
337526-97-3DP, complex with acyl carrier protein
337526-99-5P 337527-00-1P
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT 140345-60-4, DNA (Escherichia coli clone pWO114 gene fabH plus flanks) **206887-32-3**, DNA (Streptococcus pneumoniae gene fabH)
329083-57-0 338475-24-4, 1: PN: WO0130988 SEQID:17 unclaimed DNA 338475-26-6, 4: PN: WO0130988 SEQID: 19 unclaimed DNA 338475-27-7, 8: PN: WO0130988 SEQID: 23 unclaimed DNA 338475-28-8 338475-30-2 338475-31-3 338475-33-5 338475-35-7 338475-36-8 338475-37-9 338475-39-1, 23: PN: WO0130988 SEQID: 1 unclaimed DNA 338475-42-6, 26: PN: WO0130988 SEQID: 4 unclaimed DNA 338475-45-9, 29: PN: WO0130988 SEQID: 7 unclaimed DNA 338475-47-1, 31: PN: WO0130988 SEQID: 9 unclaimed DNA 338475-49-3
RL: PRP (Properties)
(unclaimed nucleotide sequence; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

IT **146890-02-0**, Protein ACP (Escherichia coli clone pMR24 gene acpP acyl-carrier) **146890-24-6 148998-18-9**, Protein (Escherichia coli clone pHAP1 gene envM reduced) **200143-22-2**
206887-31-2 315726-50-2 329083-56-9 338475-25-5 338475-29-9 **338475-32-4** 338475-34-6 338475-38-0 338475-40-4 338475-41-5 338475-43-7 338475-44-8 338475-46-0 338475-48-2 338475-50-6
RL: PRP (Properties)
(unclaimed protein sequence; screening for compds. affecting fatty acid biosynthesis and making fatty acid synthesis pathway reagents using fatty acid biosynthesis pathway enzymes)

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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(2) Kuhajda; US 5759837 A 1998 HCAPLUS
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L85 ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:911271 HCAPLUS
DN 134:52296
ED Entered STN: 29 Dec 2000
TI Staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof
IN **Kallender, Howard**; Van Horn, Stephanie; Warren, Richard L.; **Lonsdale, John**
PA Smithkline Beecham Corporation, USA; Smithkline Beecham PLC
SO PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C07H021-00
ICS C07H021-04; C12N005-00; C12N009-00; C12N015-00; C12N015-87; C12P021-06
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 7, 10
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000078780	A1	20001228	WO 2000-US16882	20000619
	W: JP				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6489139	B1	20021203	US 1999-339614	19990624
PRAI	US 1999-339614	A	19990624		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2000078780	ICM	C07H021-00
	ICS	C07H021-04; C12N005-00; C12N009-00; C12N015-00; C12N015-87; C12P021-06
US 6489139	ECLA	C07K014/31

AB FabZ polypeptides and DNA (RNA) encoding such fabZ and a procedure for producing such polypeptides by recombinant techniques is disclosed. Also disclosed are methods for utilizing such fabZ for the treatment of infection, particularly bacterial infections. Antagonists against such fabZ and their use as a therapeutic to treat infections, particularly bacterial infections are also disclosed. Also disclosed are diagnostic assays for detecting polynucleotides encoding Fab (Fatty acid biosynthesis) and for detecting the polypeptide in a host.

ST Staphylococcus gene fabZ sequence; malonylCoA ACP transacylase gene sequence

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(fabZ; staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof)

IT Vaccines
(protein fabZ; staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof)

IT Antibodies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(protein fabZ; staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof)

IT Antibacterial agents
DNA sequences
Drug screening
Molecular cloning
Protein sequences
Staphylococcus aureus
(staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof)

IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof)

IT **313561-96-5**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof)

IT **313561-97-6**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof)

IT **37257-17-3**, Malonyltransferase, [acyl carrier protein]
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(staphylococcus fabZ (malonylCoA:ACP transacylase) protein and uses thereof)

IT 195843-43-7
RL: PRP (Properties)
(unclaimed nucleotide sequence; staphylococcus fabZ (malonylCoA,ACP transacylase) protein and uses thereof)

RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Anon; EP 786519 A2 1997 HCAPLUS

L85 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 2000:814333 HCAPLUS

DN 133:360793
ED Entered STN: 21 Nov 2000
TI Bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics
IN Konstantinidis, Alexendros K.; **Lonsdale, John Timothy**; Van Aller, Glenn Scott
PA **Smithkline Beecham** Corp., USA; **Smithkline Beecham** PLC
SO PCT Int. Appl., 48 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM A61K038-51
ICS C12N009-00; C12N001-20
CC 10-1 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): 1
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000067780	A1	20001116	WO 2000-US12250	20000504
	W: JP, US				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	EP 1178820	A1	20020213	EP 2000-928847	20000504
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2003524627	T2	20030819	JP 2000-616805	20000504
	US 2003186435	A1	20031002	US 2003-443432	20030522
	US 2004087506	A1	20040506	US 2003-668588	20030923
PRAI	US 1999-132714P	P	19990506		
	WO 2000-US12250	W	20000504		
	US 2001-980875	A1	20011029		
	US 2003-443432	A1	20030522		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2000067780	ICM	A61K038-51
	ICS	C12N009-00; C12N001-20
US 2003186435	ECLA	C12N009/10C1A
US 2004087506	ECLA	C12N009/10C1A

AB Staphylococcus aureus and Streptococcus pneumoniae homologs of the fatty acid condensing enzyme gene fabH are identified by sequence homol. The genes and gene products may be of use in diagnosis and identification of the pathogen and in screening and development of novel antibiotics (no data).
ST fabH gene discovery Staphylococcus Streptococcus diagnostics therapeutics; fatty acid **condensing enzyme** Staphylococcus Streptococcus antibiotic; sequence fatty acid **condensing enzyme** Staphylococcus Streptococcus fabH gene
IT Proteins, specific or class
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); THU (Therapeutic use); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)
(ACP (acyl-carrier), S-malonyl, blocking biosynthesis of; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)
IT Infection
(Staphylococcus or Streptococcus, diagnosis of; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)
IT Vaccines
(Staphylococcus or Streptococcus, fatty acid **condensing enzyme** as antigen in; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)
IT DNA sequence analysis
Staphylococcus aureus
Streptococcus pneumoniae
(bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)
IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); THU

(Therapeutic use); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)
(**biosynthesis** of, as target for antibiotics; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT Staphylococcus
Streptococcus
(diagnosis and treatment of infection by; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(fabH; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for amplification of fabH gene of Staphylococcus or Streptococcus; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT Genetic methods
(gene discovery; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT Diagnosis
(mol., of Staphylococcus or Streptococcus infection; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT DNA sequences
(of fabH gene of Staphylococcus and Streptococcus; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT Protein sequences
(of fatty acid **condensing enzyme** of Staphylococcus and Streptococcus; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT Antibiotics
(targets for; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(to fatty acid **condensing enzyme** of Staphylococcus and Streptococcus; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT 206887-31-2 **226216-22-4**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT **9077-10-5**, **Synthase**, 3-**oxoacyl**-[**acyl carrier protein**]
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT 141-82-2D, Malonic acid, conjugates with acyl carrier protein
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); THU (Therapeutic use); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)
(blocking biosynthesis of; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)

IT **72-89-9**, Acetyl CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); THU

(Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(blocking metabolism of; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)
IT **206887-32-3**, DNA (Streptococcus pneumoniae gene fabH)
226216-23-5
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; bacterial fatty acid **condensing enzyme** genes homologous to fabH identified by gene discovery and its potential use in diagnostics and therapeutics)
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Gentry; US 5759832 A 1998 HCAPLUS
(2) Gentry; US 5783432 A 1998 HCAPLUS
(3) Gentry; US 5885572 A 1999 HCAPLUS

=> d all hitstr l84 tot

L84 ANSWER 1 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:12601 HCAPLUS
DN 134:96258
ED Entered STN: 05 Jan 2001
TI **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport
IN Pompejus, Markus; Kroger, Burkhard; Schroder, Hartwig; Zelder, Oskar; Haberhauer, Gregor
PA Basf Aktiengesellschaft, Germany
SO PCT Int. Appl., 1119 pp.
CODEN: PIXXD2
DT **Patent**
LA English
IC ICM C12N015-00
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 9, 10, 16
FAN.CNT 9

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001000805	A2	20010104	WO 2000-IB926	20000623 <--
	WO 2001000805	A3	20011025		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	BR 2000011810	A	20020507	BR 2000-11810	20000623 <--
	TR 200103708	T2	20020821	TR 2001-200103708	20000623 <--
	TR 200103707	T2	20020923	TR 2001-200103707	20000623 <--
	EP 1255839	A2	20021113	EP 2000-939001	20000623 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
	US 6696561	B1	20040224	US 2000-602787	20000623 <--
	JP 2004513603	T2	20040513	JP 2001-506799	20000623 <--
	US 2004030116	A1	20040212	US 2003-627476	20030725 <--
PRAI	US 1999-141031P	P	19990625	<--	
	DE 1999-19931454	A	19990708	<--	
	DE 1999-19931478	A	19990708	<--	
	DE 1999-19931563	A	19990708	<--	
	DE 1999-19932122	A	19990709	<--	
	DE 1999-19932124	A	19990709	<--	
	DE 1999-19932125	A	19990709	<--	
	DE 1999-19932128	A	19990709	<--	
	DE 1999-19932180	A	19990709	<--	
	DE 1999-19932182	A	19990709	<--	
	DE 1999-19932190	A	19990709	<--	
	DE 1999-19932191	A	19990709	<--	
	DE 1999-19932209	A	19990709	<--	
	DE 1999-19932212	A	19990709	<--	
	DE 1999-19932227	A	19990709	<--	
	DE 1999-19932228	A	19990709	<--	
	DE 1999-19932229	A	19990709	<--	

DE 1999-19932230	A	19990709	<--
DE 1999-19932927	A	19990714	<--
DE 1999-19933005	A	19990714	<--
DE 1999-19933006	A	19990714	<--
DE 1999-19940764	A	19990827	<--
DE 1999-19940765	A	19990827	<--
DE 1999-19940766	A	19990827	<--
DE 1999-19940830	A	19990827	<--
DE 1999-19940831	A	19990827	<--
DE 1999-19940832	A	19990827	<--
DE 1999-19940833	A	19990827	<--
DE 1999-19941378	A	19990831	<--
DE 1999-19941379	A	19990831	<--
DE 1999-19941395	A	19990831	<--
DE 1999-19942077	A	19990903	<--
DE 1999-19942078	A	19990903	<--
DE 1999-19942079	A	19990903	<--
DE 1999-19942088	A	19990903	<--
DE 1999-19930476	A	19990701	<--
DE 1999-19931415	A	19990708	<--
DE 1999-19931418	A	19990708	<--
DE 1999-19931419	A	19990708	<--
DE 1999-19931420	A	19990708	<--
DE 1999-19931424	A	19990708	<--
DE 1999-19931428	A	19990708	<--
DE 1999-19931434	A	19990708	<--
DE 1999-19931435	A	19990708	<--
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DE 1999-19931453	A	19990708	<--
DE 1999-19931457	A	19990708	<--
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DE 1999-19931541	A	19990708	<--
DE 1999-19931573	A	19990708	<--
DE 1999-19931592	A	19990708	<--
DE 1999-19931632	A	19990708	<--
DE 1999-19931634	A	19990708	<--
DE 1999-19931636	A	19990708	<--
DE 1999-19932126	A	19990709	<--
DE 1999-19932130	A	19990709	<--
DE 1999-19932186	A	19990709	<--
DE 1999-19932206	A	19990709	<--
DE 1999-19932922	A	19990714	<--
DE 1999-19932926	A	19990714	<--
DE 1999-19932928	A	19990714	<--
DE 1999-19933004	A	19990714	<--
US 2000-602787	A1	20000623	
WO 2000-IB926	W	20000623	

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2001000805	ICM	C12N015-00
JP 2004513603	FTERM	4B024/AA03; 4B024/AA05; 4B024/AA11; 4B024/AA13; 4B024/AA20; 4B024/BA72; 4B024/BA73; 4B024/BA74; 4B024/BA75; 4B024/CA03; 4B024/CA04; 4B024/CA07; 4B024/CA09; 4B024/CA12; 4B024/DA10; 4B024/EA04; 4B024/FA15; 4B024/GA14; 4B024/GA21; 4B024/HA01; 4B024/HA12; 4B063/QA01; 4B063/QA18; 4B063/QA19; 4B063/QQ03; 4B063/QQ06; 4B063/QQ43; 4B063/QR39; 4B063/QR48; 4B063/QR56; 4B063/QS34; 4B064/AB07; 4B064/AD01; 4B064/AE03; 4B064/AF01; 4B064/AF27; 4B064/AG01; 4B064/CA02; 4B064/CC24; 4B064/DA10; 4B064/DA13; 4B064/DA15; 4B065/AA24X; 4B065/AA24Y; 4B065/AA26X; 4B065/AA57X; 4B065/AA58X; 4B065/AA72X; 4B065/AA83X; 4B065/AA87X; 4B065/AA87Y; 4B065/AB01; 4B065/BA02; 4B065/BA03; 4B065/BA10; 4B065/CA05; 4B065/CA10; 4B065/CA13; 4B065/CA23; 4B065/CA24; 4B065/CA27; 4B065/CA41; 4B065/CA43; 4B065/CA44; 4B065/CA46; 4B065/CA50; 4H045/AA10; 4H045/AA20; 4H045/AA30; 4H045/BA09; 4H045/BA41; 4H045/CA11; 4H045/EA01; 4H045/EA15; 4H045/EA50; 4H045/FA74 <--

AB Three hundred thirty-eight isolated genomic nucleic acid mols., designated MCT nucleic acid mols., are described which encode novel MCT proteins from Corynebacterium glutamicum that are involved in membrane construction and membrane transport. The invention also provides antisense nucleic acid mols., recombinant expression vectors containing MCT nucleic acid mols., and

host cells into which the expression vectors have been introduced. The invention still further provides isolated MCT proteins, mutated MCT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from C. glutamicum based on genetic engineering of MCT genes in this organism. Because C. glutamicum is commonly used in the industry for the large-scale production of a variety of fine chems., the MCT nucleic acids of the invention can be used to improve the yield or production of one or more fine chems. from a Corynebacterium or Brevibacterium species. The MCT nucleic acids may also be used for diagnostic identification of an organism as being C. glutamicum or a close relative such as Corynebacterium diphtheriae, the causative agent of diphtheria.

ST membrane synthesis transport protein gene sequence **Corynebacterium**

IT Biological transport
Corynebacterium glutamicum
DNA sequences
Membrane, biological
Molecular cloning
Protein sequences
Transformation, genetic
(**Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT Gene, microbial
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(**Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(MCT (membrane construction and membrane transport); **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT Diphtheria
(diagnosis of; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT **Corynebacterium** diphtheriae
(diagnostic detection of; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT Amino acids, preparation
Aromatic compounds
Carbohydrates, preparation
Coenzymes
Enzymes, preparation
Glycols, preparation
Lipids, preparation
Nucleosides, preparation
Nucleotides, preparation
Polyketides
Proteins, general, preparation
Purine bases
Pyrimidine bases
Vitamins
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(modulation of fermentative production of; **Corynebacterium** glutamicum genes encoding proteins involved in membrane **synthesis** and membrane transport)

IT Diagnosis
(of diphtheria; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT Fermentation
(of fine chems.; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT Acids, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(organic, modulation of fermentative production of; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT **Fatty acids, preparation**
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)

(saturated, modulation of fermentative production of; **Corynebacterium** glutamicum genes encoding proteins involved in membrane **synthesis** and membrane transport)

IT Brevibacterium
Brevibacterium butanicum
Brevibacterium healii
Brevibacterium ketoglutamicum
Brevibacterium ketosoreductum
Brevibacterium linens
Brevibacterium paraffinolyticum
Corynebacterium
Corynebacterium acetoacidophilum
Corynebacterium acetoglutamicum
Corynebacterium acetophilum
Corynebacterium ammoniagenes
Corynebacterium fujiokense
Corynebacterium herculis
Corynebacterium lactofermentum
Corynebacterium nitrilophilus
Microorganism
(transfection of; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT **Fatty acids, preparation**
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(unsatd., modulation of fermentative production of; **Corynebacterium** glutamicum genes encoding proteins involved in membrane **synthesis** and membrane transport)

IT 174663-80-0 195460-94-7 314317-53-8 314317-59-4 314318-21-3
314319-28-3 314319-30-7 314322-48-0 314322-50-4 314322-52-6
314322-56-0 314323-94-9 314325-96-7 314326-02-8 314326-24-4
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318298-76-9 318298-77-0 318298-78-1 318298-79-2 318298-80-5
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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU

(Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT 318298-86-1 318298-88-3 318298-89-4 318298-90-7 318298-91-8
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318467-27-5

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT 52-90-4P, L-Cysteine, preparation 56-40-6P, Glycine, preparation 56-41-7P, L-Alanine, preparation 56-45-1P, L-Serine, preparation 56-84-8P, L-Aspartic acid, preparation 56-85-9P, L-Glutamine, preparation 56-86-0P, L-Glutamic acid, preparation 56-87-1P, L-Lysine, preparation 60-18-4P, L-Tyrosine, preparation 61-90-5P, L-Leucine, preparation 63-68-3P, L-Methionine, preparation 63-91-2P, L-Phenylalanine, preparation 71-00-1P, L-Histidine, preparation 72-18-4P, L-Valine, preparation 72-19-5P, L-Threonine, preparation 73-22-3P, L-Tryptophan, preparation 73-32-5P, L-Isoleucine, preparation 74-79-3P, L-Arginine, preparation 147-85-3P, L-Proline, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(modulation of fermentative production of; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

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(nucleotide sequence; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT 151001-60-4, PN: WO9946405 SEQID: 23 unclaimed DNA 300626-10-2
RL: PRP (Properties)
(unclaimed sequence; **corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

IT **318296-91-2**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; **Corynebacterium** glutamicum genes encoding proteins involved in membrane synthesis and membrane transport)

RN 318296-91-2 HCAPLUS
CN Protein MCT (membrane construction and membrane transport) (Corynebacterium glutamicum strain ATCC_13032 clone RXA01467) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 2 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:738565 HCAPLUS
DN 132:33613
ED Entered STN: 21 Nov 1999
TI The malonyl-CoA-long-chain acyl-CoA axis in the maintenance of mammalian cell function
AU Zammit, Victor A.
CS Cell Biochemistry, Hannah Research Institute, Ayr, KA6 5HL, UK
SO Biochemical Journal (**1999**), 343(3), 505-515
CODEN: BIJOAK; ISSN: 0264-6021

PB Portland Press Ltd.
DT Journal; General Review
LA English
CC 13-0 (Mammalian Biochemistry)
Section cross-reference(s): 2
AB A review with 149 refs. Long-chain acyl-CoA esters have potent specific actions (e.g. on gene transcription, membrane trafficking) as well as non-specific ones (e.g. on phospholipid bilayers). They are synthesized on the cytosolic aspects of several intracellular membranes, to give rise to (a) cytosolic pool(s) to which a variety of enzymes and processes have access, including some localized in the nucleus. Their concentration in cells is highly regulated, interconversion with corresponding acylcarnitines being the most important mechanism involved. This reaction is catalyzed by cytosol-accessible carnitine long-chain acyl (palmitoyl) transferase activities that are themselves located on multiple membrane systems. Regulation of these activities is through the inhibitory action of malonyl-CoA. Hence the existence of a potent malonyl-CoA-acyl-CoA axis through which many processes involved in the maintenance of mammalian cell function are regulated. The mol., topog. and physiol. interactions that make this possible are described and discussed.
ST review malonyl CoA carnitine palmitoyl transferase insulin metab membrane
IT Metabolism
(energy; malonyl-CoA-long-chain acyl-CoA axis in maintenance of mammalian energy metabolism)
IT **Lipids**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(glycerolipids; malonyl-CoA-long-chain acyl-CoA axis in **synthesis** of)
IT Cell membrane
(malonyl-CoA-long-chain acyl-CoA axis in maintenance of mammalian cell function at)
IT Oxidation
(.beta.-; malonyl-CoA-long-chain acyl-CoA axis in maintenance of mammalian energy metabolism via)
IT 9068-41-1, Carnitine palmitoyl **transferase**
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(**malonyl**-CoA-long-chain acyl-CoA axis in maintenance of mammalian cell function)
IT **524-14-1**, Malonyl-CoA
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(malonyl-CoA-long-chain acyl-CoA axis in maintenance of mammalian cell function)
IT 9004-10-8, Insulin, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(role of insulin in malonyl-CoA-long-chain acyl-CoA axis maintenance of mammalian cell function)
RE.CNT 149 THERE ARE 149 CITED REFERENCES AVAILABLE FOR THIS RECORD
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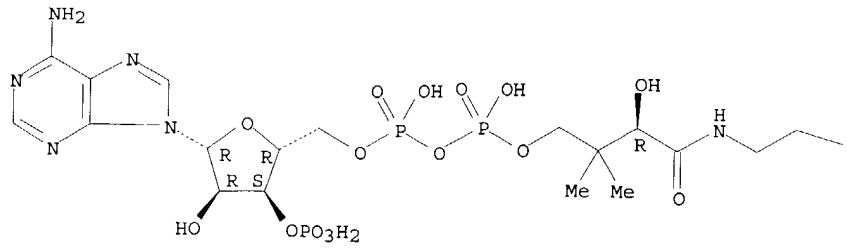
IT **524-14-1**, Malonyl-CoA
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(malonyl-CoA-long-chain acyl-CoA axis in maintenance of mammalian cell function)

RN 524-14-1 HCAPLUS

CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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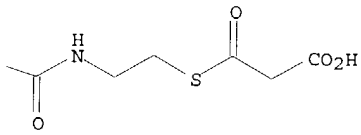

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AN 1999:486245 HCAPLUS
DN 131:225948
ED Entered STN: 06 Aug 1999
TI Co-expression of 3-**ketoacyl-ACP reductase** and polyhydroxyalkanoate synthase genes induces PHA production in Escherichia coli HB101 strain
AU Taguchi, Kazunori; Aoyagi, Yoshihiro; Matsusaki, Hiromi; Fukui, Toshiaki; Doi, Yoshiharu
CS The Institute of Physical and Chemical Research (RIKEN), Polymer Chemistry Laboratory and the RIKEN Group of Japan Science and Technology Corporation, Wako, 351-0198, Japan
SO FEMS Microbiology Letters (**1999**), 176(1), 183-190
CODEN: FMLED7; ISSN: 0378-1097
PB Elsevier Science B.V.
DT Journal
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)
AB The Escherichia coli 3-ketoacyl-ACP reductase gene (fabGEc) was cloned using a PCR technique to investigate the metabolic link between fatty acid metabolism and polyhydroxyalkanoate (PHA) production Three plasmids resp. harboring fabGEc and the poly-3-hydroxyalkanoate synthesis genes phaCAc and phaC1Ps from Aeromonas caviae and Pseudomonas sp. 61-3 resp. were constructed and introduced into E. coli HB101 strain. On a two-stage cultivation using dodecanoate as the sole carbon source, recombinant E. coli HB101 strains harboring fabGEc and phaC genes accumulated PHA copolymers (about 8 wt% of dry cell weight) consisting of several (R)-3-hydroxyalkanoate units of C4, C6, C8, and C10. It has been suggested that overexpression of the fabGEc gene leads to the supply of (R)-3-hydroxyacyl-CoA for PHA synthesis via fatty acid degradation
ST polyhydroxyalkanoate prodn fatty acid metab recombinant Escherichia; **ketoacyl acyl carrier protein reductase** polyhydroxyalkanoate formation Escherichia; synthase polyhydroxyalkanoate recombinant Escherichia; gene **ketoacyl ACP reductase** polyhydroxyalkanoate **synthase** cloning Escherichia
IT Aeromonas caviae
Escherichia coli
Molecular cloning
Pseudomonas
(co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)
IT **Fatty acids, biological studies**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(co-expression of 3-**ketoacyl-acyl-carrier**

protein reductase and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(fabG; co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

IT Polyesters, biological studies
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(hydroxycarboxylic acid-based; co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(phaC1; co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

IT Gene, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(phaC; co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

IT **37250-34-3P**, 3-**Ketoacyl-acyl-carrier protein reductase** 134688-88-3P, Polyhydroxyalkanoate synthase
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

IT 143-07-7, Dodecanoic acid, biological studies 1420-36-6, Acetoacetyl-CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

IT **85-61-0D**, CoA, (R)-3-hydroxyacyl esters 21804-29-5
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

IT 120675-91-4 147398-31-0, 3-Hydroxybutyric acid-3-hydroxyhexanoic acid copolymer
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD

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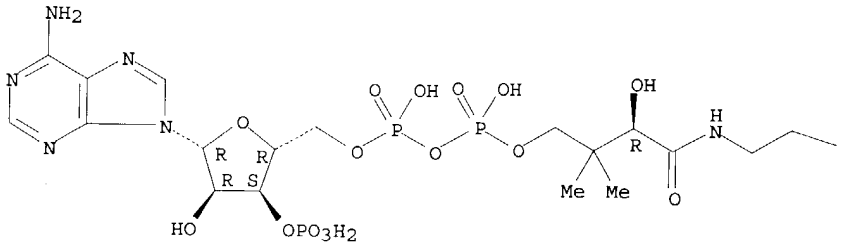
IT **37250-34-3P**, 3-**Ketoacyl-acyl-carrier protein reductase**
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)
RN 37250-34-3 HCAPLUS
CN Reductase, 3-oxoacyl- [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **85-61-0D**, CoA, (R)-3-hydroxyacyl esters
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(co-expression of 3-**ketoacyl-acyl-carrier protein reductase** and polyhydroxyalkanoate synthase genes induces polyhydroxyalkanoate production in Escherichia coli HB101)
RN 85-61-0 HCAPLUS
CN Coenzyme A (8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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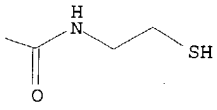


L84 ANSWER 4 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:283006 HCAPLUS
DN 124:336386
ED Entered STN: 14 May 1996
TI Inhibition of **.beta.-ketoacyl-acyl carrier protein synthase** III (FabH) by acyl-acyl carrier protein in Escherichia coli
AU Heath, Richard J.; Rock, Charles O.
CS Dep. Biochem., St. Jude Children's Res. Hosp., Memphis, TN, 38101, USA
SO Journal of Biological Chemistry (**1996**), 271(18), 10996-11000
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English

CC 7-3 (Enzymes)
Section cross-reference(s): 10

AB .beta.-Ketoacyl-acyl carrier protein (ACP) synthase III (the fabH gene product) condenses acetyl-CoA with malonyl-ACP to initiate fatty acid biosynthesis in the dissociated, type II fatty acid synthase systems typified by Escherichia coli. The accumulation of malonyl-acyl carrier protein (ACP) following the inhibition of a reconstituted fatty acid synthase system by acyl-ACP implicated synthase III (FabH) as a target for acyl-ACP regulation (Heath, R. J., and Rock, C. O. (1996) J. Biol. Chemical 271, 1833-1836); therefore, the FabH protein was purified and its biochem. and regulatory properties examined FabH exhibited a Km of 40 .mu.M for acetyl-CoA and 5 .mu.M for malonyl-ACP. FabH also accepted other acyl-CoAs as primers with the rank order of activity being acetyl-CoA .apprxeq. propionyl-CoA .mchgt. butyryl-CoA. FabH utilized neither hexanoyl-CoA nor octanoyl-CoA. Acyl-ACPs suppressed FabH activity, and their potency increased with increasing acyl chain length between 12 and 20 carbon atoms. Nonesterified ACP was not an inhibitor. Acyl-ACP inhibition kinetics were mixed with respect to acetyl-CoA, but were competitive with malonyl-ACP, indicating that acyl-ACPs decrease FabH activity by binding to either the free enzyme or the acyl-enzyme intermediate. These data support the concept that the inhibition of chain initiation at the .beta.-ketoacyl-ACP synthase III step contributes to the attenuation of fatty acid biosynthesis by acyl-ACP.

ST FabH protein inhibition acylated ACP protein; Escherichia **ketoacyl ACP synthase** III

IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(**ketoacyl-acyl carrier protein synthase** III (FabH) role in feedback regulation of fatty acid **synthesis** in Escherichia coli)

IT Molecular structure-biological activity relationship
(**ketoacyl-acyl carrier protein synthase** III-inhibiting; of long-chain acyl-acyl carrier proteins)

IT Michaelis constant
(of **ketoacyl-acyl carrier protein synthase** III of Escherichia coli)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(ACP (acyl-carrier protein), S-arachidyl; inhibition of **ketoacyl-acyl-carrier protein synthase** III (FabH) of Escherichia coli by acyl-acyl carrier proteins)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ACP (acyl-carrier protein), S-lauryl; inhibition of **ketoacyl -acyl-carrier protein synthase** III (FabH) of Escherichia coli by acyl-acyl carrier proteins)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ACP (acyl-carrier protein), S-myristyl; inhibition of **ketoacyl -acyl-carrier protein synthase** III (FabH) of Escherichia coli by acyl-acyl carrier proteins)

IT Proteins, specific or class
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(ACP (acyl-carrier protein), S-malonyl, kinetic mechanism of **ketoacyl-acyl carrier protein synthase** III inhibition by long-chain acyl-acyl carrier proteins)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(ACP (acyl-carrier protein), S-oleoyl, inhibition of **ketoacyl -acyl-carrier protein synthase** III (FabH) of Escherichia coli by acyl-acyl carrier proteins)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ACP (acyl-carrier protein), S-palmitoyl, inhibition of **ketoacyl-acyl-carrier protein synthase** III (FabH) of Escherichia coli by acyl-acyl carrier

proteins)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ACP (acyl-carrier protein), S-stearoyl, inhibition of **ketoacyl -acyl-carrier protein synthase** III (FabH) of Escherichia coli by acyl-acyl carrier proteins)

IT **9077-10-5P**
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation); PROC (Process)
(**ketoacyl-acyl-carrier protein synthase** III (FabH) of Escherichia coli characterization and inhibition by acyl-acyl carrier proteins)

IT **72-89-9**, Acetyl-CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(kinetic mechanism of **ketoacyl-acyl carrier protein synthase** III inhibition by long-chain acyl-acyl carrier proteins)

IT 317-66-8, Propionyl-CoA 2140-48-9, Butyryl-CoA.
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(specificity of **ketoacyl-acyl carrier protein synthase** III (FabH) of Escherichia coli)

IT **9077-10-5P**
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation); PROC (Process)
(**ketoacyl-acyl-carrier protein synthase** III (FabH) of Escherichia coli characterization and inhibition by acyl-acyl carrier proteins)

RN 9077-10-5 HCAPLUS
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

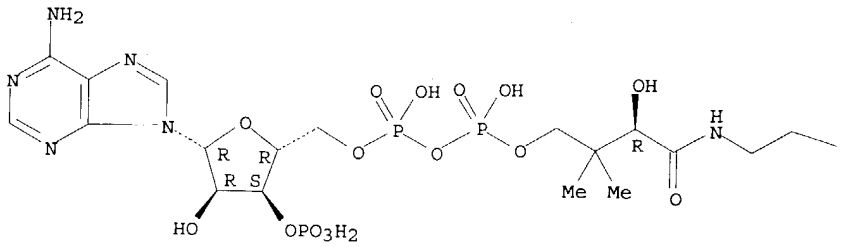
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT **72-89-9**, Acetyl-CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(kinetic mechanism of **ketoacyl-acyl carrier protein synthase** III inhibition by long-chain acyl-acyl carrier proteins)

RN 72-89-9 HCAPLUS
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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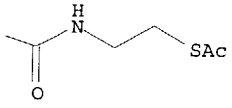


L84 ANSWER 5 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

Searched by Noble Jarrell

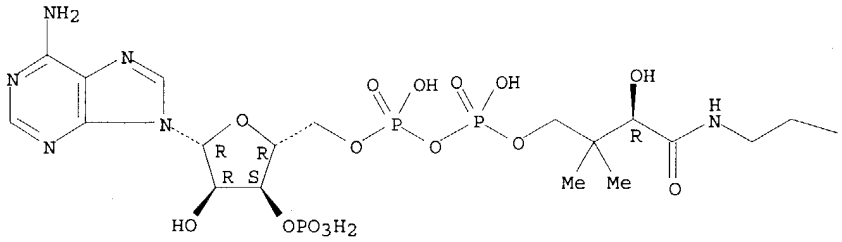
AN 1995:672981 HCAPLUS
DN 123:79243
ED Entered STN: 13 Jul 1995
TI Regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and .beta.-**ketoacyl-acyl carrier protein synthases** in Escherichia coli
AU Heath, Richard J.; Rock, Charles O.
CS Dep. Biochem., St. Jude Children's Res. Hosp., Memphis, TN, 38101, USA
SO Journal of Biological Chemistry (**1995**), 270(26), 15531-8
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Bio logy
DT Journal
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)
AB The cessation of phospholipid biosynthesis by the inhibition of the sn-glycerol-3-phosphate acyltransferase using a plsB mutant led to an accumulation of long-chain acyl-acyl carrier proteins (acyl-ACP) and the concomitant inhibition of de novo fatty acid biosynthesis in Escherichia coli. Malonyl-CoA did not accumulate when phospholipid and fatty acid synthesis was blocked. However, the inactivation of .beta.-ketoacyl-ACP synthases I and II with the antibiotic cerulenin triggered a large increase in the accumulation of malonyl-CoA following the cessation of phospholipid synthesis, illustrating that the .beta.-ketoacyl-ACP synthases were responsible for the degradation of malonyl-CoA in the presence of long-chain acyl-ACP. The acyl-ACP requirement for malonyl-CoA degradation activity was confirmed by shifting enoyl-ACP reductase mutants (fabI(Ts)) to the non-permissive temperature, leading to the abrupt cessation of fatty acid synthesis and the accumulation of malonyl-CoA in the absence of cerulenin. Anal. of the ACP pool composition before and after the temperature shift showed that the fabI block did not result in the accumulation of long-chain acyl-ACP. These data indicate a feedback regulatory loop that functions to recycle malonyl-CoA to acetyl-CoA following the down-regulation of fatty acid and phospholipid formation and provides a physiol. rational for the acyl-ACP-dependent, malonyl-ACP decarboxylase reaction catalyzed by .beta.-ketoacyl-ACP synthases I and II.
ST Escherichia malonyl CoA metab regulation; acylated ACP protein Escherichia malonyl CoA; **ketoacyl ACP synthase** Escherichia malonyl CoA
IT Escherichia coli
(regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and .beta.-**ketoacyl-acyl carrier protein synthases** in Escherichia coli)
IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(ACP (acyl-carrier protein), esters with long-chain fatty acids; regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and .beta.-**ketoacyl-acyl carrier protein synthases** in Escherichia coli)
IT **Fatty acids, biological studies**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(long-chain, esters with acyl-carrier protein; regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and .beta.-**ketoacyl-acyl carrier protein synthases** in Escherichia coli)
IT **9077-10-5**, .beta.-**Ketoacyl-acyl carrier protein synthase**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(I and II; regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and .beta.-**ketoacyl-acyl carrier protein synthases** in Escherichia coli)
IT **524-14-1**, Malonyl-CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and .beta.-**ketoacyl-acyl carrier protein synthases** in Escherichia coli)
IT **72-89-9**, Acetyl-CoA
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and .beta.-**ketoacyl-acyl carrier protein synthases** in Escherichia coli)

IT **9077-10-5, .beta.-Ketoacyl-acyl carrier protein synthase**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(I and II; regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and **.beta.-ketoacyl-acyl carrier protein synthases** in Escherichia coli)
RN 9077-10-5 HCAPLUS
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **524-14-1**, Malonyl-CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and **.beta.-ketoacyl-acyl carrier protein synthases** in Escherichia coli)
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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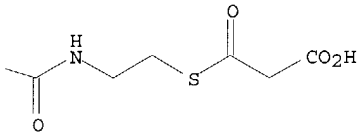
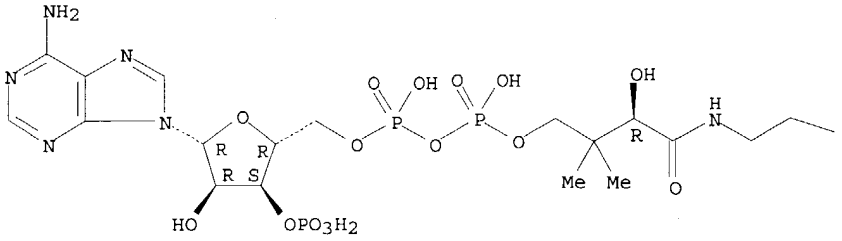


IT **72-89-9**, Acetyl-CoA
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(regulation of malonyl-CoA metabolism by acyl-acyl carrier protein and **.beta.-ketoacyl-acyl carrier protein synthases** in Escherichia coli)
RN 72-89-9 HCAPLUS
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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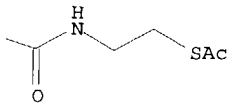


L84 ANSWER 6 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:646446 HCAPLUS
DN 119:246446
ED Entered STN: 11 Dec 1993
TI Malonyl-CoA metabolism in cardiac myocytes and its relevance to the control of fatty acid oxidation
AU Awan, M. Moneeb; Saggerson, E. David
CS Dep. Biochem. Mol. Biol., Univ. Coll. London, London, WC1E 6BT, UK
SO Biochemical Journal (**1993**), 295(1), 61-6
CODEN: BIJOAK; ISSN: 0306-3275
DT Journal
LA English
CC 13-2 (Mammalian Biochemistry)
Section cross-reference(s): 2
AB Viable myocytes were obtained from rat hearts. Oxidation of [1-14C]palmitate by these cells could be decreased by the addition of glucose (5 mM) or lactate (2 mM). In the presence of glucose, insulin decreased and adrenaline increased palmitate oxidation The myocytes contained activities of ATP citrate-lyase, acetyl-CoA carboxylase and the condensing enzyme of the fatty acid elongation system. No fatty acid synthase activity was demonstrable in myocytes. In rat hearts perfused with 5 mM glucose, malonyl-CoA content was acutely raised by insulin. In the presence of glucose + insulin, perfusion with palmitate or adrenaline decreased the malonyl-CoA content. It is concluded that malonyl-CoA can be synthesized within cardiac myocytes and that the level of this metabolite can be acutely regulated. This is likely to have consequences for the regulation of carnitine palmitoyltransferase in the heart.
ST malonyl CoA metab heart fatty acid
IT Heart, metabolism
(malonyl-CoA metabolism by myocytes of, fatty acid oxidation in relation to)
IT **Fatty acids, biological studies**
RL: RCT (Reactant); RACT (Reactant or reagent)
(oxidation of, by heart myocytes, malonyl CoA metabolism in relation to)
IT Receptors
RL: BIOL (Biological study)
(adrenergic, fatty acid oxidation by heart myocytes regulation by)
IT Fatty acids, esters
RL: BIOL (Biological study)
(long-chain, with CoA and carnitine, of heart myocytes, adrenaline and insulin and palmitate effect on)
IT **524-14-1**, Malonyl-CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by heart myocytes, fatty acid oxidation regulation in relation to)
IT 9023-93-2, Acetyl-CoA carboxylase 9027-95-6, ATP citrate-lyase **9077-10-5**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(of heart myocytes)
IT 57-10-3, Palmitic acid, biological studies
RL: RCT (Reactant); RACT (Reactant or reagent)
(oxidation of, by heart myocytes, malonyl CoA metabolism in relation to)
IT 51-43-4, Adrenaline 9004-10-8, Insulin, biological studies
RL: BIOL (Biological study)
(palmitate oxidation response to, in heart myocytes in presence of glucose)
IT 50-21-5, Lactic acid, biological studies 50-99-7, Glucose, biological studies
RL: BIOL (Biological study)
(palmitate oxidation response to, in heart myocytes, malonyl-CoA in relation to)
IT **524-14-1**, Malonyl-CoA

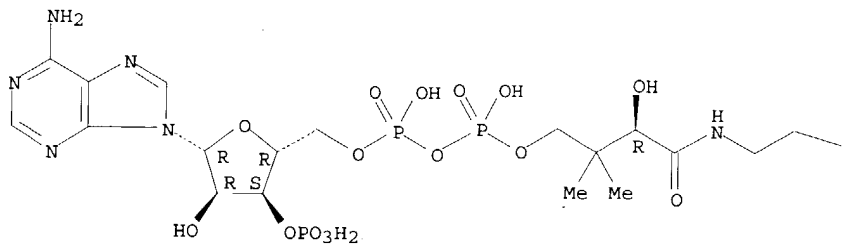
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by heart myocytes, fatty acid oxidation regulation in relation to)

RN 524-14-1 HCAPLUS

CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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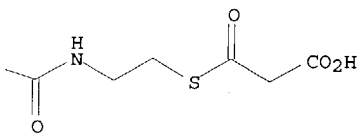


IT **9077-10-5**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(of heart myocytes)

RN 9077-10-5 HCAPLUS

CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 7 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 1993:468178 HCAPLUS

DN 119:68178

ED Entered STN: 21 Aug 1993

TI Acetyl-acyl carrier protein is not a major intermediate in fatty acid biosynthesis in spinach

AU Jaworski, Jan G.; Post-Beittenmiller, Dusty; Ohlrogge, John B.

CS Chem. Dep., Miami Univ., Oxford, OH, 45056, USA

SO European Journal of Biochemistry (**1993**), 213(3), 981-7
CODEN: EJBCAI; ISSN: 0014-2956

DT Journal

LA English

CC 11-2 (Plant Biochemistry)

AB The extent to which acety-acyl carrier protein (acetyl-ACP) is an intermediate in fatty acid biosynthesis was examined Acetyl-ACP was the least effective primer of fatty acid synthesis by spinach exts. when compared to acetyl-CoA, butyryl-ACP or hexanoyl-ACP. Furthermore, the rate of acetyl-ACP-primed fatty acid synthesis was inhibited significantly by cerulenin, indicating that the slow utilization of acetyl-ACP was predominantly by 3-oxoacyl-ACP synthase I. In light-incubated isolated chloroplasts with high rates of fatty acid synthesis (> 800 nmol.cntdot.h-1.cntdot.mg chlorophyll-1), the rate of acetyl-ACP metabolism was at least 10-30-fold slower than the rate of butyryl-ACP metabolism The relatively slow metabolism of acetyl-ACP provided in situ evidence that (a) butyryl-ACP was formed principally from condensation of malonyl-ACP with acetyl-CoA and (b) acetyl-ACP was a minor participant in fatty acid biosynthesis.

ST acetyl ACP intermediate fatty acid spinach

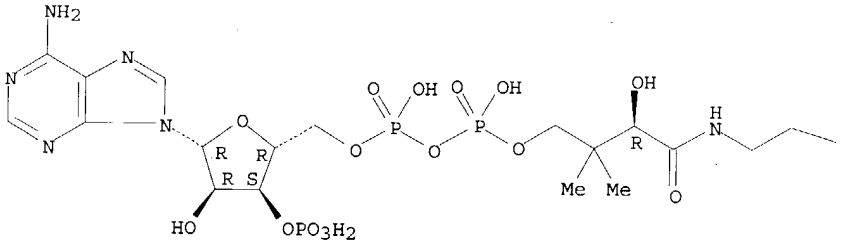
IT Light
(acetyl-ACP of spinach response to, fatty acids formation in relation to)

IT Spinach
(fatty acids formation in, acetyl-acyl carrier proteins in relation to)
IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(formation of, in spinach, acetyl-acyl carrier proteins in relation to)
IT Proteins, specific or class
RL: BIOL (Biological study)
(ACP (acyl-carrier protein), S-acyl, fatty acid formation in spinach in relation to)
IT **9077-10-5**, 3-**Oxoacyl-ACP synthase**
RL: BIOL (Biological study)
(acetyl-acyl carrier proteins role in fatty acid formation in spinach in relation to)
IT **72-89-9**, Acetyl-CoA
RL: BIOL (Biological study)
(in fatty acid formation in spinach, acetyl-ACP in relation to)
IT **9077-10-5**, 3-**Oxoacyl-ACP synthase**
RL: BIOL (Biological study)
(acetyl-acyl carrier proteins role in fatty acid formation in spinach in relation to)
RN 9077-10-5 HCAPLUS
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

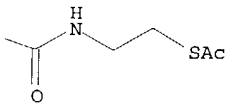
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **72-89-9**, Acetyl-CoA
RL: BIOL (Biological study)
(in fatty acid formation in spinach, acetyl-ACP in relation to)
RN 72-89-9 HCAPLUS
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



L84 ANSWER 8 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:648642 HCAPLUS
DN 117:248642
ED Entered STN: 26 Dec 1992
TI Regulation of plant fatty acid biosynthesis. Analysis of acyl-coenzyme A and acyl-acyl carrier protein substrate pools in spinach and pea chloroplasts
AU Post-Beittenmiller, Dusty; Roughan, Grattan; Ohlrogge, John B.
CS Dep. Bot. Plant Pathol., Michigan State Univ., East Lansing, MI, 48824-1312, USA
SO Plant Physiology (**1992**), 100(2), 923-30
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
CC 11-2 (Plant Biochemistry)
AB The CoA and short chain acyl-CoA pools, including acetyl- and malonyl-CoA,

in isolated spinach and pea (Pisum sativum) chloroplasts were studied. In addition, the relationships of the acetyl- and malonyl-CoA pools to the acetyl- and malonyl-ACP pools were evaluated. Essentially all of the CoA (31-54 .mu.M) in chloroplasts freshly isolated from light-grown spinach leaves or pea seedling was in the form of acetyl-CoA. Chloroplasts contained at least 77% of the total leaf acetyl-CoA, based on comparison of acetyl-CoA levels in chloroplasts and total leaf. CoA-SH was not detected either in freshly isolated chloroplasts or in incubated chloroplasts and is, therefore, less than 2 .mu.M in the stroma. The malonyl-CoA:ACP transacylase reaction is near equilibrium in both light- and dark-incubated chloroplasts, whereas the acetyl-CoA:ACP transacylase reaction is far from equilibrium in light-incubated chloroplasts. However, the acetyl-CoA:ACP transacylase reaction comes nearer to equilibrium when chloroplasts are incubated in the dark. Malonyl-CoA and -ACP could be detected in isolated chloroplasts only during light incubations, and increased with increased rates of fatty acid biosynthesis. In contrast, both acetyl-CoA and acetyl-ACP were detectable in the absence of fatty acid biosynthesis, and acetyl-ACP decreased with increased rates of fatty acid biosynthesis. Together these data have provided direct in situ evidence that acetyl-CoA carboxylase plays a regulatory role in chloroplast fatty acid biosynthesis.

ST chloroplast fatty acid formation regulation

IT Pea
Spinach
(fatty acid formation in chloroplast of, regulation of)

IT Chloroplast
(fatty acid formation in, regulation of)

IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(formation of, in chloroplast)

IT Proteins, specific or class
RL: BIOL (Biological study)
(ACP (acyl-carrier protein), of chloroplast, fatty acid formation in relation to)

IT **72-89-9**, Acetyl CoA **524-14-1**, Malonyl CoA
RL: BIOL (Biological study)
(in fatty acid formation, in chloroplast)

IT 9023-93-2, Acetyl CoA carboxylase **37257-16-2 37257-17-3**
RL: BIOL (Biological study)
(of chloroplast, fatty acid formation in relation to)

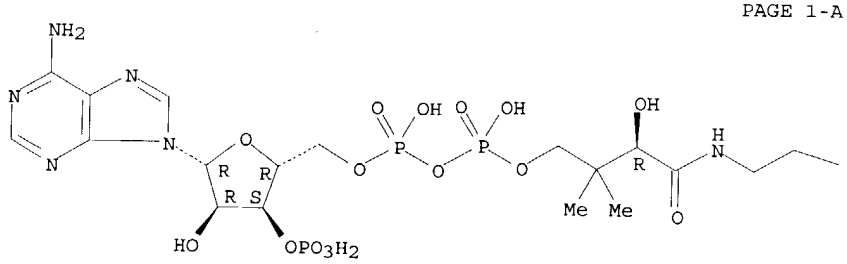
IT **72-89-9**, Acetyl CoA **524-14-1**, Malonyl CoA
RL: BIOL (Biological study)
(in fatty acid formation, in chloroplast)

RN 72-89-9 HCAPLUS

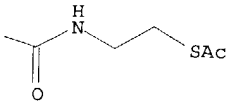
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B

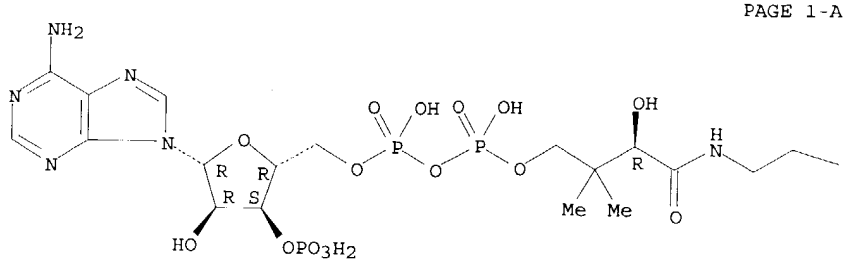


RN 524-14-1 HCAPLUS

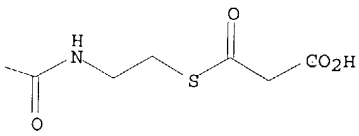
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IT **37257-16-2 37257-17-3**
RL: BIOL (Biological study)
(of chloroplast, fatty acid formation in relation to)
RN 37257-16-2 HCAPLUS
CN Acetyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37257-17-3 HCAPLUS
CN Malonyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 9 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:228021 HCAPLUS
DN 116:228021
ED Entered STN: 13 Jun 1992
TI Coenzyme acetylation and activity of the enzymes of lipogenesis in the mouse liver treated with pantetheine during streptozotocin-induced diabetes
AU Omel'yanchik, S. N.; Gurinovich, V. A.
CS Inst. Biokhim., Grodno, USSR
SO Eksperimental'naya Meditsina (Riga) (**1991**), 27, 98-103
CODEN: EKMEDL
DT Journal
LA Russian
CC 1-10 (Pharmacology)
AB The effects of pantetheine on liver levels of CoA, acyl-CoA pattern, and lipogenic enzymes were studied in mice with diabetes mellitus. The levels of total CoA and short- and long-chain acyl-CoA esters were increased with concurrent inhibition of lipogenesis. Pantetheine pretreatment (63 .mu.mol/kg s.c. 6 h prior to streptozotocin prevented the diabetes-associated changes.
ST diabetes liver acyl CoA lipogenesis pantetheine
IT Liver, metabolism
(acyl-CoA and lipogenesis in, pantetheine effects on, in diabetes mellitus)
IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(formation of, by liver, pantetheine effects on, in diabetes mellitus)
IT Diabetes mellitus
(liver acyl-CoA and lipogenesis responses to pantetheine in)
IT 16816-67-4
RL: BIOL (Biological study)
(liver acyl-CoA and lipogenesis responses to, in diabetes mellitus)
IT **85-61-0D**, CoA, acyl esters 2226-71-3, Phosphopantetheine

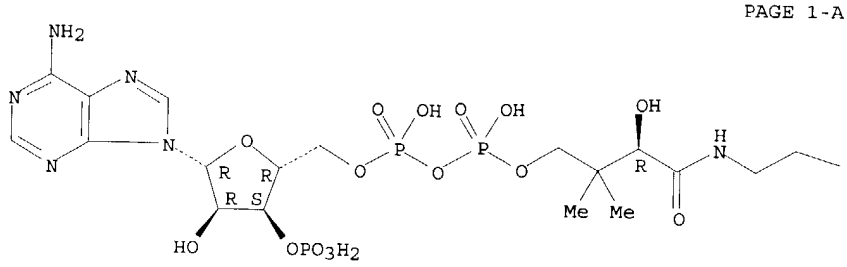
3633-59-8, Dephospho-CoA 9012-31-1, Acetyl-CoA synthetase 9045-77-6, Fatty acid synthetase **37257-16-2**
RL: BIOL (Biological study)
(of liver, pantetheine effects on, in diabetes mellitus)

IT **85-61-0D**, CoA, acyl esters **37257-16-2**
RL: BIOL (Biological study)
(of liver, pantetheine effects on, in diabetes mellitus)

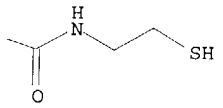
RN 85-61-0 HCAPLUS
CN Coenzyme A (8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



RN 37257-16-2 HCAPLUS
CN Acetyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 10 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1991:180461 HCAPLUS
DN 114:180461
ED Entered STN: 17 May 1991
TI Evidence against cytochrome b5 involvement in liver microsomal fatty acid elongation
AU Demirkapi, Nursel; Carreau, Jean Paul; Ghesquier, Daniele
CS Hop. Bicetre, Le Kremlin-Bicetre, 94275, Fr.
SO Biochimica et Biophysica Acta (**1991**), 1082(1), 49-56
CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English
CC 6-1 (General Biochemistry)
Section cross-reference(s): 7, 13
AB This study provides strong evidence against cytochrome b5 participation in the first reduction step-.beta.-ketoredn. of rat liver microsomal fatty acid chain elongation. .beta.-Ketoreductase was not inducible by diet conditions since its activity was the same in microsomes from fasted rats and in rats fed a fat-free diet. Consequently, its activity was appreciable in microsomes from fasted rats. Nevertheless, cytochrome b5 reoxidn. rate was not stimulated by adding .beta.-ketopalmitoyl-CoA to the latter microsomes. This suggests that it is not the activated .beta.-ketoreductase which stimulates the cytochrome b5 reoxidn. rate, but another electron acceptor. The .DELTA.9-desaturase, present in microsomes from rats fed a fat-free diet, was totally inhibited by 4 mM KCN; .beta.-ketopalmitoyl-CoA or malonyl-CoA stimulated the reoxidn. rate of cytochrome b5 but this increase was also inhibited by 4 mM KCN. This suggests that .DELTA.9-desaturase is involved in the stimulation and shows that any inhibitor of .DELTA.9-desaturase, including cytochrome b5 antibodies, may induce elongation inhibition. NADH-dependent .beta.-ketoreductase activity was partially purified from Triton X-100 solubilized microsomes, in a fraction essentially free of cytochrome b5.

Furthermore, when the fraction containing cytochrome b5 and NADH-cytochrome-b5 reductase was added to the fraction containing .beta.-ketoreductase activity, no increase in .beta.-ketoreductase activity was observed Stearoyl-CoA desaturase activity which is also present in microsomes from rats fed a fat-free diet led to the results which have been misinterpreted in the conclusions of previous studies.

ST liver microsome fatty acid elongation cytochrome; cytochrome b5 fatty acid elongation microsome

IT Electron exchange
(by cytochrome b5 of liver microsome, fatty acid elongation in relation to)

IT Liver, metabolism
(fatty acid chain elongation in microsome of, cytochrome b5 in relation to)

IT Microsome
(fatty acid chain elongation in, of liver, cytochrome b5 in relation to)

IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(long-chain, formation of, chain elongation in, in liver microsome, cytochrome b5 in relation to)

IT 9014-34-0
RL: BIOL (Biological study)
(cytochrome b5 interaction with, of liver microsome, fatty acid elongation in relation to)

IT **524-14-1**, Malonyl-coenzyme A 34619-89-1, .beta.-Ketopalmitoyl-coenzyme A
RL: BIOL (Biological study)
(cytochrome b5 of liver microsome stimulation by, desaturase in, fatty acid elongation in relation to)

IT 9035-39-6, Cytochrome b5
RL: BIOL (Biological study)
(desaturase interaction with, of liver microsome, fatty acid elongation in relation to)

IT 9028-40-4P, **.beta.-Ketoacyl**-coenzyme A **reductase**
RL: PREP (Preparation)
(of liver microsome, purification and characterization of, cytochrome b5 in relation to)

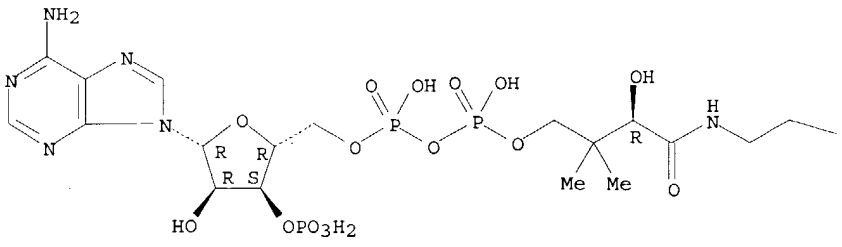
IT **524-14-1**, Malonyl-coenzyme A
RL: BIOL (Biological study)
(cytochrome b5 of liver microsome stimulation by, desaturase in, fatty acid elongation in relation to)

RN 524-14-1 HCAPLUS

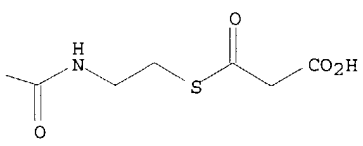
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B

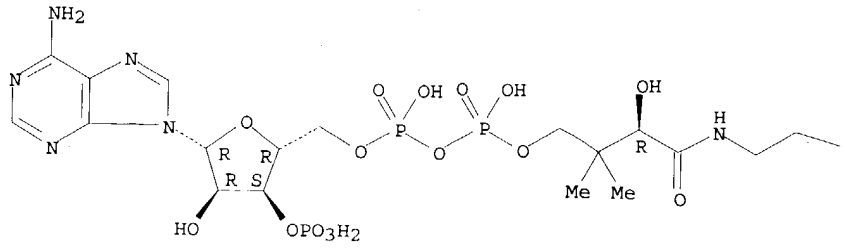


Searched by Noble Jarrell

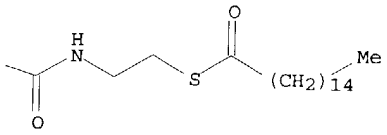
L84 ANSWER 11 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1990:626496 HCAPLUS
DN 113:226496
ED Entered STN: 22 Dec 1990
TI Low fatty acid elongation rate in the presence of NADH in the liver endoplasmic reticulum. Overinhibition by BSA at the .beta.-ketoreductase level
AU Demirkapi, Nursel; Ghesquier, Daniele
CS Hop. Bicetre, Le Kremlin-Bicetre, 94275, Fr.
SO Biochimica et Biophysica Acta (**1990**), 1046(2), 229-32
CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English
CC 6-1 (General Biochemistry)
Section cross-reference(s): 7, 13
AB The rate of NADH-dependent palmitoyl-CoA elongation was only 41% of that of NADH-dependent elongation in microsomes from rats fed a fat-free diet, in the absence of BSA. This value was markedly lowered to 5%, when the assay was performed in the presence of BSA. The determination of the intermediate products showed that 93% of the total products accumulated as .beta.-ketostearate in the presence of BSA and NADH, whereas the accumulated .beta.-ketostearate was only 25% of the total products in the presence of BSA and NADPH. BSA was shown to be responsible for the low rate of NADH-dependent elongation by inhibiting the .beta.-ketoreductase in the presence of NADH and, thereby, inducing .beta.-ketostearate accumulation. These results indicate that NADH is probably not the physiol. electron donor to the elongation pathway.
ST fatty acid elongation NADH albumin liver; ketoreductase inhibition albumin endoplasmic reticulum liver
IT Liver, metabolism
(fatty acid NADH-dependent elongation in endoplasmic reticulum of, albumin effect on, ketoreductase inhibition in relation to)
IT Endoplasmic reticulum
(fatty acid elongation in, of liver, albumin effect on, ketoreductase inhibition in relation to)
IT Albumins, biological studies
RL: BIOL (Biological study)
(fatty acid formation by endoplasmic reticulum of liver in NADH presence response to, ketoreductase inhibition in relation to)
IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(formation of, by endoplasmic reticulum of liver in NADH presence, albumin effect on, ketoreductase inhibition in relation to)
IT **1763-10-6**, Palmitoyl-COA
RL: BIOL (Biological study)
(NADH-dependent elongation of, in endoplasmic reticulum of liver, albumin effect on, ketoreductase inhibition in relation to)
IT 58-68-4, NADH
RL: BIOL (Biological study)
(fatty acid elongation by liver endoplasmic reticulum in presence of, albumin effect on, ketoreductase inhibition in relation to)
IT 16694-29-4P, .beta.-Ketostearic acid
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(formation of, in endoplasmic reticulum of liver in NADH presence, albumin effect on, ketoreductase inhibition in relation to)
IT **37250-34-3**
RL: BIOL (Biological study)
(inhibition of, of endoplasmic reticulum of liver by albumin, fatty acid elongation in the presence of NADH in relation to)
IT 53-57-6, NADPH
RL: BIOL (Biological study)
(ketoreductase of endoplasmic reticulum of liver response to, albumin effect on, NADH-dependent fatty acid elongation in relation to)
IT **1763-10-6**, Palmitoyl-COA
RL: BIOL (Biological study)
(NADH-dependent elongation of, in endoplasmic reticulum of liver, albumin effect on, ketoreductase inhibition in relation to)
RN 1763-10-6 HCAPLUS
CN Coenzyme A, S-hexadecanoate (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IT **37250-34-3**
RL: BIOL (Biological study)
(inhibition of, of endoplasmic reticulum of liver by albumin, fatty acid elongation in the presence of NADH in relation to)
RN 37250-34-3 HCAPLUS
CN Reductase, 3-oxoacyl- [acyl carrier protein] (9CI) (CA INDEX NAME)

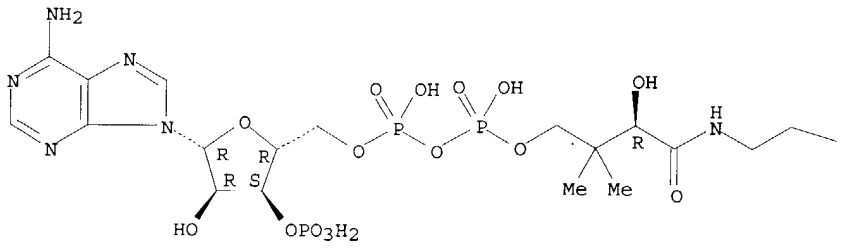
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 12 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1990:116668 HCAPLUS
DN 112:116668
ED Entered STN: 31 Mar 1990
TI Enzyme site-specific changes in hepatic microsomal fatty acid chain elongation in streptozotocin-induced diabetic rats
AU Suneja, Sanoj K.; Osei, Peter; Cook, Lynda; Nagi, Mahmoud N.; Cinti, Dominick L.
CS Health Cent., Univ. Connecticut, Farmington, CT, USA
SO Biochimica et Biophysica Acta (**1990**), 1042(1), 81-5
CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English
CC 14-8 (Mammalian Pathological Biochemistry)
AB The hepatic microsomal fatty acid chain elongation of palmitoyl-CoA and .gamma.-linolenoyl-CoA was diminished by 40-50% in male Sprague-Dawley rats made diabetic for 2 and 4 wk following the i.v. administration of a single dose (65 mg/kg) of streptozotocin. Anal. of the activities of the 4 enzymic components showed that only 1 enzyme, the condensing enzyme, which catalyzes the initial and rate-limiting step in chain elongation, was altered by the diabetic state. Both chain elongation and condensation activities were depressed to the same extent, whereas .beta.-ketoacyl-CoA reductase, .beta.-hydroxyacyl-CoA dehydrase and trans-2-enoyl-CoA reductase activities were the same as the values obtained with nondiabetic controls. Two-week administration of 10 units of insulin per day to rats which were diabetic for a 2-wk period resulted in the reversal of the reduced palmitoyl-CoA elongation and condensation activities to control values. However, neither the condensation nor the elongation of .gamma.-linolenoyl-CoA was reversed by the insulin treatment. These results support the notion of multiple condensing enzymes or chain elongation systems.
ST liver fatty acid elongation diabetes insulin
IT **Fatty acids, biological studies**
RL: BIOL (Biological study)
(elongation of, in liver microsomes, defect of, in diabetes mellitus, insulin effect on)
IT Liver, metabolism
(fatty acid chain elongation by microsomes of, defect in, in diabetes, insulin effect on)

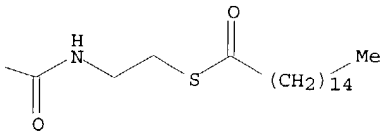
IT Diabetes mellitus
(fatty acid chain elongation defect in liver in, insulin effect on)
IT Microsome
(fatty acid elongation by hepatic, defect in, in diabetes mellitus, insulin effect on)
IT Enzymes
RL: BIOL (Biological study)
(fatty acid-elongating, of liver microsomes, in diabetes mellitus, insulin effect on)
IT **1763-10-6**, Palmitoyl-CoA 27843-61-4, .gamma.-Linolenoyl-CoA
RL: BIOL (Biological study)
(elongation of, in liver microsomes, defect of, in diabetes mellitus, insulin effect on)
IT 9004-10-8, Insulin, biological studies
RL: BIOL (Biological study)
(fatty acid elongation defect response to, of liver in diabetes)
IT 9027-13-8, .beta.-Hydroxyacyl-CoA dehydrase **9077-10-5**, **Condensing enzyme** 91755-85-0, NADPH-dependent trans-2-enoyl-CoA reductase 125268-64-6, NADPH-dependent **.beta.-ketoacyl-CoA reductase**
RL: BIOL (Biological study)
(of liver microsomes, in diabetes mellitus, insulin effect on)
IT **1763-10-6**, Palmitoyl-CoA
RL: BIOL (Biological study)
(elongation of, in liver microsomes, defect of, in diabetes mellitus, insulin effect on)
RN 1763-10-6 HCAPLUS
CN Coenzyme A, S-hexadecanoate (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IT **9077-10-5**, **Condensing enzyme**
RL: BIOL (Biological study)
(of liver microsomes, in diabetes mellitus, insulin effect on)
RN 9077-10-5 HCAPLUS
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

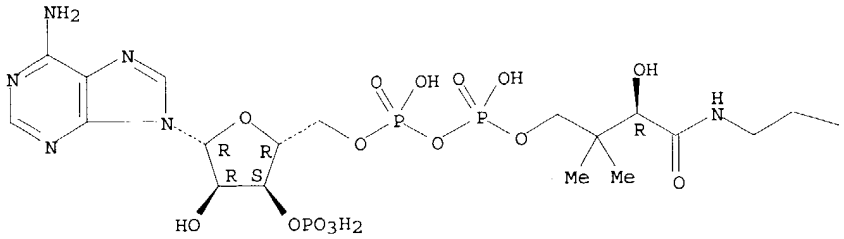
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 13 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:571557 HCAPLUS
DN 111:171557
ED Entered STN: 10 Nov 1989
TI Existence of acetyl-CoA-dependent chain elongation system in hepatic peroxisomes of rat: effects of clofibrate and di-(2-ethylhexyl)phthalate on the activity
AU Horie, Shuichi; Suzuki, Toshinari; Suga, Tetsuya
CS Dep. Clin. Biochem., Tokyo Coll. Pharm., Hachioji, 192-03, Japan
SO Archives of Biochemistry and Biophysics (**1989**), 274(1), 64-73

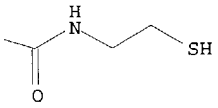
CODEN: ABBIA4; ISSN: 0003-9861
DT Journal
LA English
CC 13-2 (Mammalian Biochemistry)
AB The acetyl-CoA-dependent elongation of medium-chain acyl-CoA in the presence of pyridine nucleotide was studied in rat liver. The activity was increased by the administration of the peroxisome proliferators, clofibrate and di-(2-ethylhexyl)phthalate, and the change was more remarkable in peroxisomes than in mitochondria. Addition of 0.01% Triton X 100 to the incubation mixture increased the mitochondrial activity, whereas the peroxisomal activity did not increase. The pH optimum for the peroxisomal activity was in the range of pH 6.5-7.0 and that for the mitochondrial activity was pH 7.5-8.0. The specificities of primer chain length in both organelles were almost the same, and octanoyl-CoA was the preferred substrate. Peroxisomal activity was completely inhibited by the addition of 1 mM N-ethylmaleimide or 1 mM p-hydroxymercuribenzoic acid, whereas the activity did not change on the addition of 1 mM KCN or an antibody to acyl-CoA oxidase, the 1st enzyme of the peroxisomal .beta.-oxidation system. The activity of enoyl-CoA reductase, which catalyzes the last step of the elongation system, was also detected in peroxisomes, although the main activity was localized in microsomes. When the liver peroxisomal fraction of clofibrate-treated rats was incubated with a mixture of octanoyl-CoA, acetyl-CoA, NADH, NADPH, and Triton X 100 in a buffer system, dodecanoyl-CoA was detected as the main product by radio-gas chromatog. On the other hand, the elongation activity was decreased greatly by the addition of NAD+ into the mixture Thus, peroxisomes have activity to elongate medium chain acyl-CoA. The peroxisomal elongation system may consist of the reverse reaction of the .beta.-oxidation system except for the last step, which is catalyzed by enoyl-CoA reductase. The peroxisomal elongation system is less active than the .beta.-oxidation system under physiol. conditions.
ST liver peroxisome fatty acid chain elongation
IT **Fatty acids, biological studies**
RL: BIOL (Biological study)
(elongation of, in mitochondria and peroxisomes of liver)
IT Liver, metabolism
(fatty acid chain elongation by mitochondria and peroxisomes of)
IT Peroxisome
(fatty acid chain elongation system of, of liver, mitochondrial system in relation to)
IT Mitochondria
(fatty acid chain elongation system of, of liver, peroxisome system in relation to)
IT Cell nucleus
Microsome
(fatty acid-metabolizing enzymes of, of liver)
IT **85-61-0D**, CoA, medium-chain fatty acid esters 1264-52-4, Octanoyl-CoA
RL: BIOL (Biological study)
(elongation of, acetyl CoA dependence of, in liver peroxisome)
IT 110-86-1D, Pyridine, nucleotides
RL: BIOL (Biological study)
(fatty acid chain elongation by liver peroxisome dependence on)
IT 6244-92-4, Dodecanoyl-CoA
RL: FORM (Formation, nonpreparative)
(formation of, from octanyl-CoA by liver peroxisome)
IT **72-89-9**, Acetyl CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by liver peroxisome)
IT 9001-05-2, Catalase 9001-46-1, Glutamate dehydrogenase 9023-03-4, Cytochrome c reductase **37251-09-5** 61116-22-1, Acyl CoA-oxidase
RL: BIOL (Biological study)
(of liver subcellular fractions)
IT **85-61-0D**, CoA, medium-chain fatty acid esters
RL: BIOL (Biological study)
(elongation of, acetyl CoA dependence of, in liver peroxisome)
RN 85-61-0 HCAPLUS
CN Coenzyme A (8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



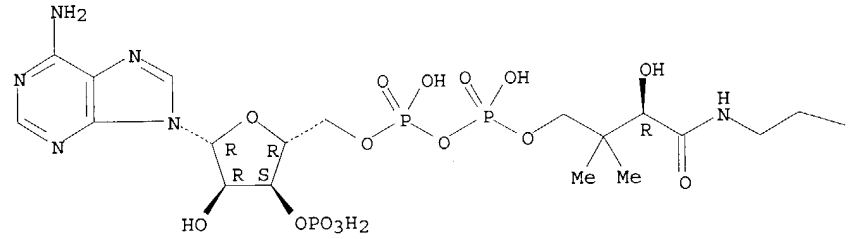
PAGE 1-B



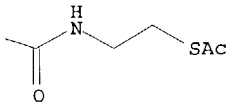
IT **72-89-9**, Acetyl CoA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by liver peroxisome)
RN 72-89-9 HCAPLUS
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IT **37251-09-5**
RL: BIOL (Biological study)
(of liver subcellular fractions)
RN 37251-09-5 HCAPLUS
CN Reductase, enoyl-[acyl carrier protein] (reduced nicotinamide adenine dinucleotide phosphate) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

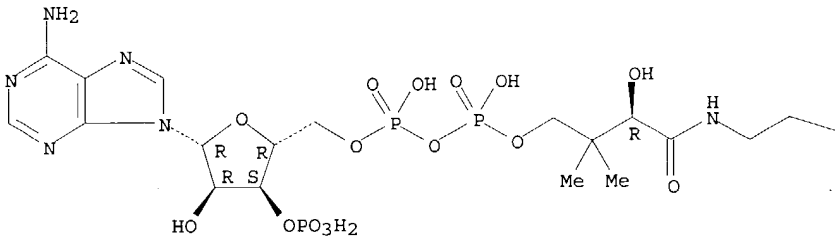
L84 ANSWER 14 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:530800 HCAPLUS
DN 111:130800

ED Entered STN: 14 Oct 1989
TI Comparison of glycerolipid biosynthesis in non-green plastids from sycamore (Acer pseudoplatanus) cells and cauliflower (Brassica oleracea) buds
AU Alban, Claude; Joyard, Jacques; Douce, Roland
CS Dep. Rech. Foundam., Cent. Etud. Nucl. Grenoble, Grenoble, F-38041, Fr.
SO Biochemical Journal (**1989**), 259(3), 775-83
CODEN: BIJOAK; ISSN: 0306-3275
DT Journal
LA English
CC 11-2 (Plant Biochemistry)
Section cross-reference(s): 7
AB The availability of methods to fractionate nongreen plastids and to prepare their limiting envelope membranes (Alban, C., et al., 1988) allowed a detailed anal. of the biosynthesis of lysophosphatidic acid, phosphatidic acid, diacylglycerol, and monogalactosyldiacylglycerol (MGDG) in 2 different types of nongreen starch-containing plastids: plastids isolated from cauliflower buds and amyloplasts isolated from sycamore cells. An enzyme (acyl-ACP (acyl carrier protein):sn-glycerol 3-phosphate acyltransferase) recovered in the soluble fraction of nongreen plastids transfers oleic acid from oleoyl-ACP to the sn-1 position of sn-glycerol 3-phosphate to form lysophosphatidic acid. Then a membrane-bound enzyme (acyl-ACP:monoacyl-sn-glycerol 3-phosphate acyltransferase), localized in the envelope membrane, catalyzes the acylation of the available sn-2 position of 1-oleoyl-sn-glycerol 3-phosphate by palmitic acid from palmitoyl-ACP. Therefore, both the soluble phase and the envelope membranes are necessary for acylation of sn-glycerol 3-phosphate. The major difference between cauliflower and sycamore membranes is the very low level of phosphatidate phosphatase activity in sycamore envelope membrane. Therefore, very little diacylglycerol is available for MGDG synthesis in sycamore, compared with cauliflower. These findings are consistent with the similarities and differences described in lipid metabolism of mature chloroplasts from C18:3 and C16:3 plants (those with MGDG containing C18:3 and C16:3 fatty acids). Sycamore contains only C18 fatty acids in MGDG, and the envelope membranes from sycamore amyloplasts have a low phosphatidate phosphatase activity and therefore the enzymes of the Kornberg-Pricer pathway have a low efficiency of incorporation of sn-glycerol 3-phosphate into MGDG. By contrast, cauliflower contains MGDG with C16:3 fatty acid, and the incorporation of sn-glycerol 3-phosphate into MGDG by the enzymes associated with envelope membranes is not limited by the phosphatidate phosphatase. These results demonstrate that: (1) nongreen plastids employ the same biosynthetic pathway as that previously established for chloroplasts (the formation of glycerolipids is a general property of all plastids, chloroplasts as well as nongreen plastids), (2) the envelope membranes are the major structure responsible for the biosynthesis of phosphatidic acid, diacylglycerol, and MGDG, and (3) the enzymes of the envelope Kornberg-Pricer pathway have the same properties in nongreen starch-containing plastids as in mature chloroplasts from C16:3 and C18:3 plants.
ST glycerolipid formation plastid sycamore cauliflower
IT Lysophosphatidic acids
Phosphatidic acids
RL: FORM (Formation, nonpreparative)
(formation of, in nongreen plastids of cauliflower and sycamore)
IT Cauliflower
(glycerolipid formation in plastids of)
IT Plastid
(glycerolipids formation in, of cauliflower)
IT **Fatty acids, biological studies**
RL: BIOL (Biological study)
(of envelope galactolipids, of cauliflower and sycamore plastids)
IT Proteins, specific or class
RL: BIOL (Biological study)
(ACP (acyl-carrier protein), S-oleoyl, in glycerolipid formation in nongreen plastids)
IT Proteins, specific or class
RL: BIOL (Biological study)
(ACP (acyl-carrier protein), S-palmitoyl, in glycerolipid formation in nongreen plastids)
IT Plastid
(amylo-, glycerolipid formation in, of sycamore)
IT Glycerides, biological studies
RL: FORM (Formation, nonpreparative)
(di-, formation of, in nongreen plastids of cauliflower and sycamore)
IT Glycerides, biological studies
RL: FORM (Formation, nonpreparative)

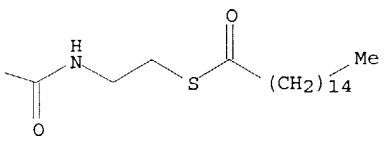
(di-, digalactosyl, formation of, in nongreen plastids of cauliflower and sycamore)
IT Glycerides, biological studies
RL: FORM (Formation, nonpreparative)
(di-, monogalactosyl, formation of, in nongreen plastids of cauliflower and sycamore)
IT Lipids, biological studies
RL: FORM (Formation, nonpreparative)
(glycero-, formation of, in nongreen plastids from cauliflower and sycamore)
IT Maple
(A. pseudoplatanus, glycerolipid formation in amyloplasts of)
IT **1763-10-6**
RL: BIOL (Biological study)
(acyl transferase specificity in cauliflower plastid envelope in relation to)
IT 17989-41-2, sn-Glycerol 3-phosphate
RL: RCT (Reactant); RACT (Reactant or reagent)
(acylation of, in glycerolipid formation in nongreen plastids)
IT 65528-98-5, 1-Oleoyl-sn-glycerol 3-phosphate
RL: RCT (Reactant); RACT (Reactant or reagent)
(formation and acylation of, in nongreen plastids)
IT 2298-57-9
RL: FORM (Formation, nonpreparative)
(formation of, in nongreen plastids)
IT 2956-16-3
RL: BIOL (Biological study)
(glycerol phosphate incorporation into plastid envelope lipids response to, in cauliflower and sycamore)
IT 57-10-3, Palmitic acid, biological studies 112-80-1, 9-Octadecenoic acid (Z)-, biological studies
RL: BIOL (Biological study)
(in glycerolipid formation in nongreen plastids)
IT 9025-77-8, Phosphatidate phosphatase
RL: BIOL (Biological study)
(of cauliflower and sycamore nongreen plastids, glycerolipid formation in relation to)
IT **113066-34-5**
RL: BIOL (Biological study)
(of nongreen plastids, glycerolipid formation in relation to)
IT **1763-10-6**
RL: BIOL (Biological study)
(acyl transferase specificity in cauliflower plastid envelope in relation to)
RN 1763-10-6 HCAPLUS
CN Coenzyme A, S-hexadecanoate (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



Searched by Noble Jarrell

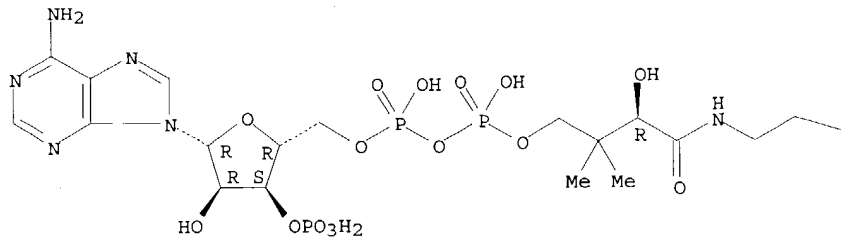
IT **113066-34-5**
RL: BIOL (Biological study)
(of nongreen plastids, glycerolipid formation in relation to)
RN 113066-34-5 HCAPLUS
CN Acyltransferase, acyl-[acyl carrier protein]-glycerol phosphate (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

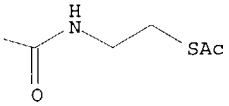
L84 ANSWER 15 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:228509 HCAPLUS
DN 110:228509
ED Entered STN: 25 Jun 1989
TI Acetoacetyl-acyl carrier protein synthase. A target for the antibiotic thiolactomycin
AU Jackowski, Suzanne; Murphy, Cynthia M.; Cronan, John E., Jr.; Rock, Charles O.
CS Dep. Biochem., St. Jude Child. Res. Hosp., Memphis, TN, 38101, USA
SO Journal of Biological Chemistry (**1989**), 264(13), 7624-9
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
CC 10-5 (Microbial Biochemistry)
Section cross-reference(s): 7
AB The biochem. basis for the inhibition of fatty acid biosynthesis in Escherichia coli by the antibiotic thiolactomycin was investigated. A biochem. assay was developed to measure acetoacetyl-acyl carrier protein (ACP) synthase activity, a 3rd condensing enzyme from E. coli. In contrast to the other 2 condensing enzymes, acetoacetyl-ACP synthase (synthase III) condensed malonyl-ACP with acetyl-CoA, rather than with acetyl-ACP. The concentration dependence of thiolactomycin inhibition of fatty acid biosynthesis in vivo was the same as the inhibition of acetoacetyl-ACP synthase activity in vitro, indicating that the 2 phenomena were related. A thiolactomycin-resistant mutant (strain CDM5) was isolated. The specific activity of acetoacetyl-ACP synthase in exts. from this mutant was 10-fold lower than in exts. from its thiolactomycin-sensitive parent, resulting in a marked defect in the ability of strain CDM5 to incorporate acetyl-CoA into fatty acids in vitro. The residual acetoacetyl-ACP synthase activity in the resistant strain was refractory to thiolactomycin inhibition. In addition, acetyl-CoA:ACP transacylase activity in strain CDM5 was resistant to inactivation by thiolactomycin, suggesting that the acetoacetyl-ACP synthase also catalyzes this transacylation reaction. These data point to acetoacetyl-ACP synthase as a target for thiolactomycin inhibition of bacterial fatty acid biosynthesis.
ST thiolactomycin acetoacetyl ACP synthase Escherichia
IT Escherichia coli
(acetoacetyl-acyl carrier protein synthase of, as thiolactomycin target)
IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(formation of, mechanism of thiolactomycin inhibition of, in Escherichia coli)
IT Proteins, specific or class
RL: BIOL (Biological study)
(ACP (acyl-carrier protein), S-malonyl, condensation with acetyl-CoA, by acetoacetyl-acyl carrier protein synthase of Escherichia coli)
IT 82079-32-1, Thiolactomycin
RL: BIOL (Biological study)
(acetoacetyl-acyl carrier protein synthase of Escherichia coli inhibition by)
IT **72-89-9**, Acetyl-CoA
RL: BIOL (Biological study)
(malonyl-ACP condensation with, by acetoacetyl-acyl carrier protein synthase of Escherichia coli)
IT **109456-65-7**, Acetoacetyl-acyl carrier protein synthase
RL: PROC (Process)
(thiolactomycin inhibition of, of Escherichia coli)
IT **72-89-9**, Acetyl-CoA
RL: BIOL (Biological study)
(malonyl-ACP condensation with, by acetoacetyl-acyl carrier protein synthase of Escherichia coli)
RN 72-89-9 HCAPLUS
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IT **109456-65-7**, Acetoacetyl-acyl carrier protein synthase
RL: PROC (Process)
(thiolactomycin inhibition of, of Escherichia coli)
RN 109456-65-7 HCAPLUS
CN Synthetase, acetoacetyl- [acyl carrier protein] (9CI) (CA INDEX NAME)

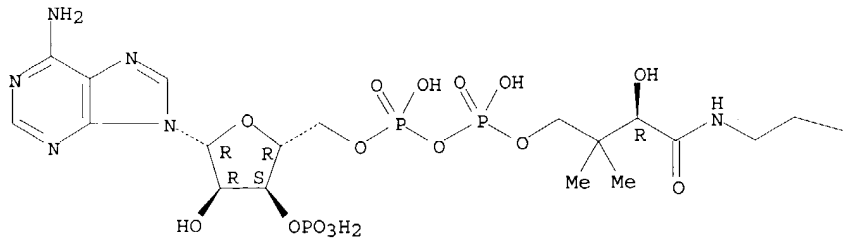
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 16 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:107643 HCAPLUS
DN 110:107643
ED Entered STN: 03 Apr 1989
TI Action of Ebselen on rat hepatic microsomal enzyme-catalyzed fatty acid chain elongation, desaturation, and drug biotransformation
AU Laguna, Juan C.; Nagi, Mahmoud N.; Cook, Lynda; Cinti, Dominick L.
CS Health Cent., Univ. Connecticut, Farmington, CT, 06032, USA
SO Archives of Biochemistry and Biophysics (**1989**), 269(1), 272-83
CODEN: ABBIA4; ISSN: 0003-9861
DT Journal
LA English
CC 1-4 (Pharmacology)
AB In the previous study, the organoselenium-containing anti-inflammatory agent, Ebselen, was found to disrupt both hepatic microsomal NADH- and NADPH-dependent electron transport chains. In the current investigation, the focus is on the action of Ebselen on three sep. metabolic reactions, namely, fatty acid chain elongation, desatn., and drug biotransformation, which utilize reducing equivalent via these microsomal electron transport pathways. Both NADH-dependent and NADPH-dependent chain elongation reactions showed (i) that the condensation step was inhibited by Ebselen; all 3 substrates, palmitoyl CoA (16:0), palmitoleoyl CoA (16:1), and .gamma.-linolenyl CoA (18:3), were differentially affected by Ebselen; for example, the apparent Ki's of Ebselen for the condensation of 16:0, 16:1, and 18:3 in the absence of bovine serum albumin (BSA) preincubation were 7, 14, and 34 .mu.M, and those in the presence of BSA preincubation were 35, 62, and 150 .mu.M, resp., supporting earlier data for multiple condensing enzymes; (ii) that the .beta.-ketoacyl CoA reductase-catalyzed reaction step which appears to receive electrons, at least in part, from the cytochrome b5 system, was also markedly inhibited by varying Ebselen concns.; and (iii) that similar results were obtained with the dehydrase and the enoyl CoA reductase. Hence, each of the 4 component steps was significantly inhibited by Ebselen. Another important fatty acid biotransformation reaction, .DELTA.9 desatn. of stearoyl CoA to oleoyl CoA, was significantly inhibited (90%) by 30 .mu.M Ebselen. This effect appeared to be directly related to the NADH-dependent electron transport chain rather than to a direct action on the desaturase enzyme. Last, Ebselen also inhibited both aminopyrine and benzphetamine N-demethylations, 2 cytochrome P 450-catalyzed reactions, in untreated rats, in rats on a high carbohydrate diet, and in phenobarbital-treated

rats.
ST Ebselen interaction liver microsome enzyme; drug metab enzyme liver microsome Ebselen; fatty acid metab enzyme liver Ebselen; electron transport chain liver microsome Ebselen
IT **Fatty acids, biological studies**
RL: BIOL (Biological study)
(desatn. and chain elongation of, Ebselen effect on hepatic microsomal enzymes catalyzing)
IT Microsome
(drug- and fatty acid-metabolizing enzymes of liver, Ebselen effect on)
IT Liver, composition
(drug- and fatty acid-metabolizing enzymes of, Ebselen effect on)
IT Drug interactions
(of ebselen, with liver microsomal drug and fatty acid metabolism)
IT Kinetics, enzymic
(of inhibition, of fatty acid chain-elongating enzymes, by Ebselen)
IT Electron transport system, biological
(of liver microsomes, Ebselen effect on)
IT Enzymes
RL: PROC (Process)
(drug-metabolizing, inhibition of, of liver microsomes, by Ebselen)
IT Enzymes
RL: PROC (Process)
(fatty acid-elongating, inhibition of, of liver microsomes, by Ebselen)
IT 53-57-6, NADPH 58-68-4, NADH
RL: BIOL (Biological study)
(Ebselen effect on hepatic microsomal enzyme-catalyzed fatty acid and drug metabolism in relation to)
IT 18198-76-0, Palmitoleoyl CoA 27843-61-4
RL: BIOL (Biological study)
(condensation of, by liver microsomes, Ebselen inhibition of)
IT 362-66-3, Stearoyl CoA
RL: BIOL (Biological study)
(conversion of, to oleoyl CoA, by liver microsomes, Ebselen inhibition of)
IT **524-14-1**, Malonyl CoA **1763-10-6**, Palmitoyl CoA
RL: BIOL (Biological study)
(cytochrome b5 reoxidn. stimulation by, in liver microsomes, Ebselen effect on)
IT 35106-50-4, .beta.-Hydroxypalmitoyl CoA
RL: FORM (Formation, nonpreparative)
(formation of, as .beta.-ketopalmitoyl CoA metabolite, by liver microsomes, Ebselen effect on)
IT 9014-34-0 9027-13-8 9028-40-4, **.beta.-Ketoacyl** CoA **reductase** 9037-69-8, Aminopyrine N-demethylase 37237-40-4, Benzphetamine N-demethylase 77649-64-0, trans-2-Enoyl CoA reductase
RL: PROC (Process)
(inhibition of, of liver microsomes, by Ebselen)
IT 60940-34-3, Ebselen
RL: BIOL (Biological study)
(liver microsomal enzyme-catalyzed fatty acid chain elongation and desatn. and drug metabolism response to)
IT 34619-89-1
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by liver microsomes, Ebselen inhibition of)
IT 9035-51-2, Cytochrome P450, biological studies
RL: BIOL (Biological study)
(of liver microsome, Ebselen effect on)
IT 4460-95-1, trans-2-Hexadecenoyl CoA 105831-42-3 119340-99-7
RL: RCT (Reactant); RACT (Reactant or reagent)
(reduction of, by liver microsomes, Ebselen inhibition of)
IT 9035-39-6, Cytochrome b5
RL: BIOL (Biological study)
(reoxidn. of microsomal, malonyl CoA-stimulated, Ebselen effect on)
IT **1716-06-9**, Oleoyl CoA
RL: BIOL (Biological study)
(stearoyl CoA conversion to, by liver microsomes, Ebselen inhibition of)
IT **524-14-1**, Malonyl CoA **1763-10-6**, Palmitoyl CoA
RL: BIOL (Biological study)
(cytochrome b5 reoxidn. stimulation by, in liver microsomes, Ebselen effect on)
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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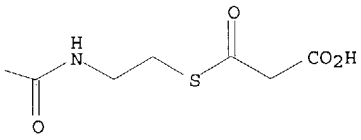
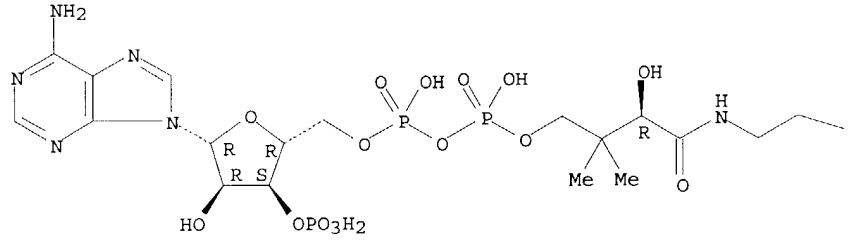


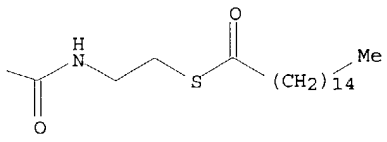
RN 1763-10-6 HCAPLUS
CN Coenzyme A, S-hexadecanoate (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



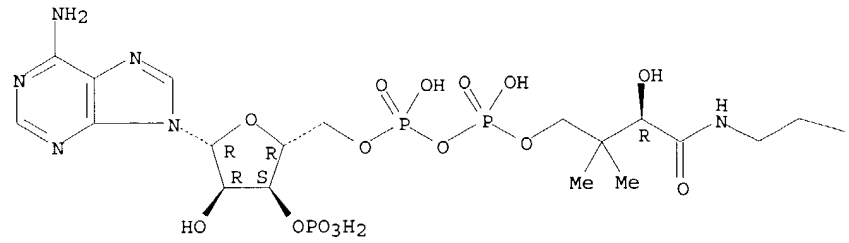
PAGE 1-B



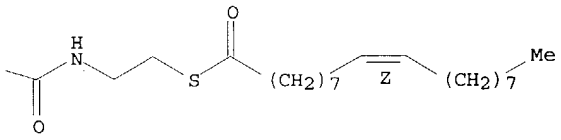
IT **1716-06-9**, Oleoyl CoA
RL: BIOL (Biological study)
(stearoyl CoA conversion to, by liver microsomes, Ebselen inhibition of)
RN 1716-06-9 HCAPLUS
CN Coenzyme A, S-(9Z)-9-octadecenoate (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

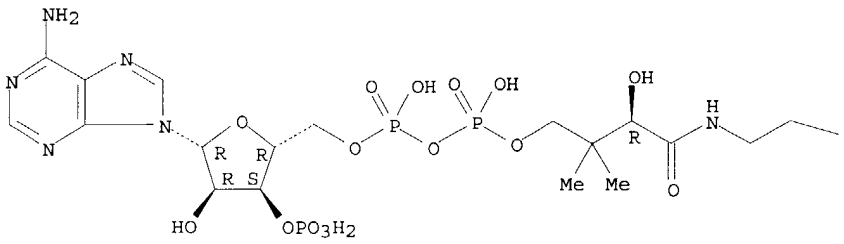


L84 ANSWER 17 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1987:100461 HCAPLUS
DN 106:100461
ED Entered STN: 05 Apr 1987
TI Study of some factors controlling fatty acid oxidation in liver mitochondria of obese Zucker rats
AU Clouet, Pierre; Henninger, Catherine; Bezard, Jean
CS Lab. Physiol. Anim. Nutr., Fac. Sci. Mirande, Dijon, 21004, Fr.
SO Biochemical Journal (**1986**), 239(1), 103-8
CODEN: BIJOAK; ISSN: 0306-3275
DT Journal
LA English
CC 14-15 (Mammalian Pathological Biochemistry)
AB Livers of genetically obese Zucker rats showed, compared with lean controls, hypertrophy and enrichment in triacylglycerols, indicating that fatty acid metabolism was directed towards lipogenesis and esterification rather than towards fatty acid oxidation Mitochondrial activities of cytochrome c oxidase and monoamine oxidase were lower when expressed per g wet weight of liver, whereas peroxisomal activities of urate oxidase and palmitoyl-CoA-dependent NAD+ reduction were unchanged. Liver mitochondria were able to oxidize oleic acid at the same rate in both obese and lean rats. For reactions occurring inside the mitochondria, e.g. octanoate oxidation and palmitoyl-CoA dehydrogenase, no difference was found between both phenotypes. Total carnitine palmitoyl-, octanoyl- and acetyl-transferase activities were slightly higher in mitochondria from obese rats, whereas the carnitine content of both liver tissue and mitochondria was lower in obese rats compared with their lean littermates. The carnitine palmitoyltransferase I activity was slightly higher in liver mitochondria from obese rats, but this enzyme was more sensitive to malonyl-CoA inhibition in obese than in lean rats. Thus, the impaired fatty acid oxidation observed in the whole liver of obese rats is probably due to the diminished transport of fatty acids across the mitochondrial inner membrane via the carnitine palmitoyltransferase I. This effect could be reinforced by the decreased mitochondrial content per g wet weight of liver. The depressed fatty acid oxidation may explain in part the lipid infiltration of liver observed in obese Zucker rats.
ST fatty acid oxidn liver mitochondria obesity; Zucker rat fatty acid oxidn liver
IT Liver, metabolism
(fatty acid oxidation by mitochondria of, of obese Zucker rat, factors controlling)
IT Rat
(fatty acid oxidation in liver mitochondria of Zucker, factors controlling)
IT Mitochondria
(fatty acid oxidation in, of liver of obese Zucker rat, factors controlling)

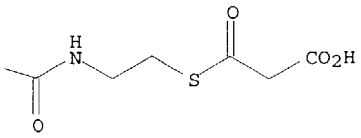
IT Lipids, biological studies
RL: FORM (Formation, nonpreparative)
(formation of, by liver of obese Zucker rat, fatty acid oxidation in relation to)
IT Peroxisome
(of liver, of obese Zucker rat, fatty acid oxidation in relation to)
IT **Fatty acids, biological studies**
RL: RCT (Reactant); RACT (Reactant or reagent)
(oxidation of, in liver mitochondria in obese Zucker rat, factors controlling)
IT Enzymes
RL: BIOL (Biological study)
(fatty acid-oxidizing, of liver, of obese Zucker rat, fatty acid oxidation in relation to)
IT Obesity
(genetic, fatty acid oxidation in liver mitochondria in, in Zucker rat, factors controlling)
IT 9068-41-1
RL: BIOL (Biological study)
(I, of liver, of obese Zucker rat, fatty acid oxidation in relation to)
IT **524-14-1, Malonyl-CoA**
RL: BIOL (Biological study)
(carnitine **acyltransferase** sensitivity to, hepatic fatty acid oxidation in obese Zucker rat in relation to)
IT 541-15-1, Carnitine 9001-05-2 9001-16-5, Cytochrome c oxidase 9001-66-5, Monoamine oxidase 9002-12-4, Urate oxidase 9012-60-6, Fatty acid oxidase 9029-90-7, Carnitine acetyltransferase 39369-19-2, Carnitine octanoyl transferase 39386-49-7, Carnitine acyltransferase
RL: BIOL (Biological study)
(of liver, of obese Zucker rat, fatty acid oxidation in relation to)
IT 112-80-1, Oleic acid, biological studies
RL: RCT (Reactant); RACT (Reactant or reagent)
(oxidation of, by liver mitochondria of obese Zucker rat, factors controlling)
IT **524-14-1, Malonyl-CoA**
RL: BIOL (Biological study)
(carnitine **acyltransferase** sensitivity to, hepatic fatty acid oxidation in obese Zucker rat in relation to)
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A

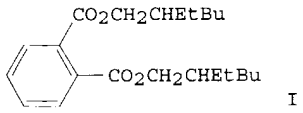


PAGE 1-B



L84 ANSWER 18 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1986:492601 HCAPLUS
DN 105:92601
ED Entered STN: 19 Sep 1986
TI Effect of the peroxisomal proliferator di(2-ethylhexyl) phthalate on

component reactions of the rat hepatic microsomal fatty acid chain elongation system and on other hepatic lipogenic enzymes
AU Prasad, M. Renuka; Cinti, Dominick L.
CS Health Cent., Univ. Connecticut, Farmington, CT, 06032, USA
SO Archives of Biochemistry and Biophysics (**1986**), 248(2), 479-88
CODEN: ABBIA4; ISSN: 0003-9861
DT Journal
LA English
CC 4-3 (Toxicology)
GI



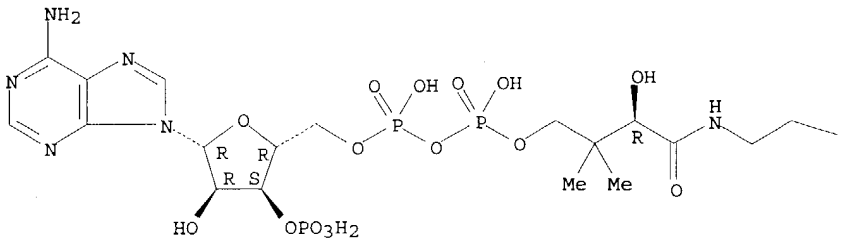
I

AB The feeding of 2% DEHP (I) [117-81-7] to rats increased the hepatic microsomal elongation rate of palmitoyl-CoA [**1763-10-6**] by .apprx.2-fold, while those of palmitoleoyl-CoA [18198-76-0] and .gamma.-linolenoyl-CoA [27843-61-4] decreased to 83 and 63%, resp., of the control values. When component reactions of the elongation pathway were measured, it was observed that only the activity of condensing enzyme was increased 2-fold, while those of .beta.-ketostearoyl-CoA reductase [**37250-34-3**], .beta.-hydroxypalmitoyl-CoA dehydrase [**37237-39-1**], and trans-2-hexadecenoyl-CoA reductase [77649-64-0] were not affected. Furthermore, the time course for induction of both condensation and elongation of palmitoyl-CoA was similar. In vitro addition of I had no effect on either condensation or elongation. Thus, the peroxisomal proliferator induces only the condensing enzyme which is the regulatory and rate-limiting step of elongation sequence. The I treatment also enhanced the cytosolic NADPH [53-57-6]-generating activities of glucose-6-phosphate dehydrogenase [9001-40-5] (2.2-fold) and malic enzyme [9028-47-1] (7.3-fold). Unexpectedly, the activities of fatty acid synthetase [9045-77-6] and citrate cleavage enzyme [9012-83-3] were unaffected. These results are discussed in light of the fact that these lipogenic enzymes are coordinately induced by diet or hormones.
ST DEHP liver microsome lipid metab
IT Liver, toxic chemical and physical damage
(DEHP toxicity to, liver microsome lipid metabolism response to)
IT **Fatty acids, biological studies**
RL: BIOL (Biological study)
(elongation of, in liver microsomes, DEHP hepatotoxicity in relation to)
IT Liver, metabolism
(hepatocyte, lipid metabolism in microsomes of, DEHP hepatotoxicity effect on)
IT Enzymes
RL: BIOL (Biological study)
(lipid-forming, of liver microsomes, DEHP hepatotoxicity in relation to)
IT 9001-40-5 9028-47-1
RL: BIOL (Biological study)
(NADPH formation in liver microsomes by, DEHP hepatotoxicity in relation to)
IT **1763-10-6** 18198-76-0 27843-61-4
RL: PRP (Properties)
(elongation rate of, in liver microsomes, DEHP hepatotoxicity effect on)
IT 53-57-6
RL: FORM (Formation, nonpreparative)
(formation of, in liver microsomes, by glucose phosphate dehydrogenase and malic enzyme, DEHP hepatotoxicity in relation to)
IT 9012-83-3 9045-77-6 **37237-39-1 37250-34-3**
77649-64-0
RL: BIOL (Biological study)
(of liver microsomes, DEHP hepatotoxicity in relation to)
IT 117-81-7
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(toxicity of, to liver, liver microsome lipid metabolism response to)
IT **1763-10-6**
RL: PRP (Properties)
(elongation rate of, in liver microsomes, DEHP hepatotoxicity effect

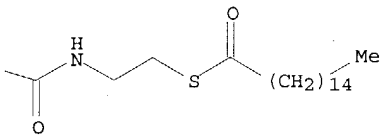
on)
RN 1763-10-6 HCAPLUS
CN Coenzyme A, S-hexadecanoate (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IT **37237-39-1 37250-34-3**
RL: BIOL (Biological study)
(of liver microsomes, DEHP hepatotoxicity in relation to)
RN 37237-39-1 HCAPLUS
CN Dehydratase, 3-hydroxyacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37250-34-3 HCAPLUS
CN Reductase, 3-oxoacyl- [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

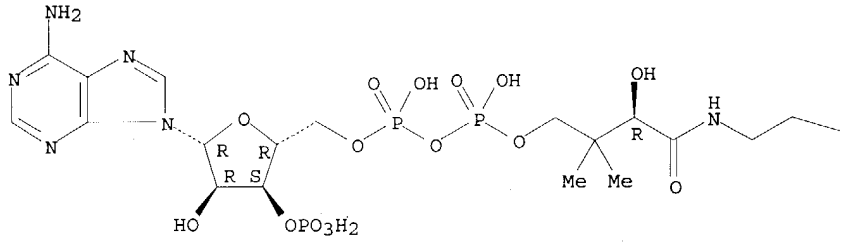
L84 ANSWER 19 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1983:212905 HCAPLUS
DN 98:212905
ED Entered STN: 12 May 1984
TI Modifications of stearoyl-CoA and stearoyl-ACP synthetase activities of leek epidermal cells by stearoyl-CoA and ACP
AU Lessire, Rene; Moreau, Patrick; Cassagne, Claude
CS Inst. Biochim. Cell. Neurochim., Bordeaux, 33077, Fr.
SO Physiologie Vegetale (**1982**), 20(4), 691-702
CODEN: PHYVAP; ISSN: 0031-9368
DT Journal
LA English
CC 11-2 (Plant Biochemistry)
Section cross-reference(s): 7
AB The study of stearoyl-CoA formation in leek (Allium porrum) epidermal cell microsomes, over different incubation periods, for 5 stearoyl-CoA concns., showed an inhibition of stearoyl-CoA synthetase. At 40-200 .mu.M, the percentage inhibition increased from 8 to 52% for an incubation time of 15 min. The inhibition measured for the stearoyl-CoA was higher than that observed in presence of malonyl-CoA or palmitoyl-CoA. The stearoyl-CoA inhibition was studied at different stearate concns. and with increasing amts. of microsomal proteins. The results obtained after preincubation of microsomes with stearoyl-CoA indicated that the inhibition of stearoyl-CoA is noncompetitive. In this same range of stearoyl-CoA concentration, the formation of stearoyl-ACP was stimulated <3-fold. The influence of ACP (acyl-carrier protein) addition on the stearoyl-CoA synthetase at different incubation times and for different concns. of CoA showed an increase of stearoyl-CoA synthesis.
ST fatty acid formation leek stearoyl synthetase
IT Leek
(stearoyl-ACP and stearoyl-CoA synthetases of, modification of)

IT Proteins
RL: BIOL (Biological study)
(acyl-carrier, stearic acid derivs., stearoyl-CoA formation in leek epidermal cells response to)
IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(long-chain, formation of, stearoyl-ACP and stearoyl-CoA synthetase modification in relation to, in leek epidermal cells)
IT 57-11-4D, acyl-carrier protein derivs. 362-66-3
RL: FORM (Formation, nonpreparative)
(formation of, in leek epidermal cells, modification of)
IT 9013-18-7 **61701-20-0**
RL: PROC (Process)
(of leek epidermal cells, modification of)
IT **524-14-1 1763-10-6**
RL: BIOL (Biological study)
(stearoyl-CoA formation in leek epidermal cells response to)
IT **61701-20-0**
RL: PROC (Process)
(of leek epidermal cells, modification of)
RN 61701-20-0 HCAPLUS
CN Synthetase, acyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

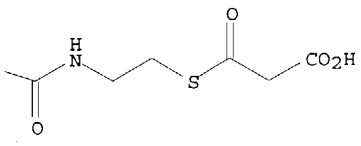
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **524-14-1 1763-10-6**
RL: BIOL (Biological study)
(stearoyl-CoA formation in leek epidermal cells response to)
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



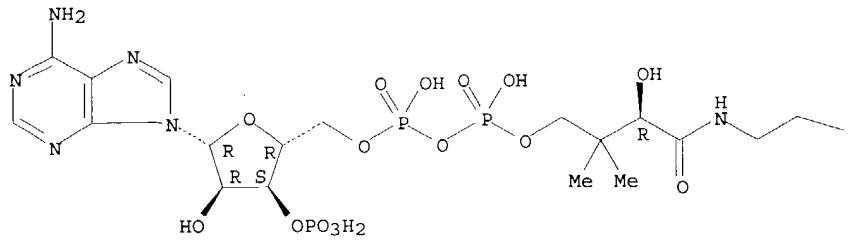
PAGE 1-B



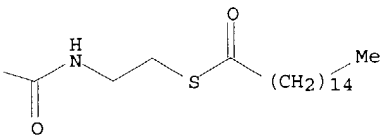
RN 1763-10-6 HCAPLUS
CN Coenzyme A, S-hexadecanoate (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



L84 ANSWER 20 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1983:156935 HCAPLUS
DN 98:156935
ED Entered STN: 12 May 1984
TI The purification and function of acetyl coenzyme A:acyl carrier protein transacylase
AU Shimakata, Takashi; Stumpf, Paul K.
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA
SO Journal of Biological Chemistry (**1983**), 258(6), 3592-8
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
CC 7-2 (Enzymes)
Section cross-reference(s): 11
AB When individual enzyme activities of the fatty acid synthetase (FAS) system were assayed in exts. from 5 different plant tissues, acyl carrier protein (ACP) acetyltransferase (I) and .beta.-ketoacyl-ACP synthetases I and II had consistently low specific activities in comparison with the other enzymes of the system. However, 2 of these exts. synthesized significant levels of medium-chain fatty acids (rather than C16 and C18 acids) from [14C]malonyl-CoA; these exts. had elevated levels of I. To explore the role of I more carefully, this enzyme was purified .apprx.180-fold from spinach leaf exts. Varying concns. of I were then added either to spinach leaf exts. or to a completely reconstituted FAS system consisting of highly purified enzymes. The results suggested that: (a) I was the enzyme catalyzing the rate-limiting step in the plant FAS system; (b) increasing concentration of I markedly increased the levels of the medium chain fatty acids, whereas increase of the other enzymes of the FAS system led to increased levels of stearic acid synthesis; and (c) .beta.-ketoacyl-ACP synthetase I was not involved in the rate-limiting step. Modulation of the activity of I may have important implications in the type of fatty acid synthesized, as well as the amount of fatty acids formed.
ST acyl carrier protein acetyltransferase spinach; fatty acid formation plant tissue
IT Spinach
([acyl carrier protein] acetyltransferase of)
IT Pea
(fatty acid formation by leaves of)
IT Cuphea lutea
Rape
Safflower
(fatty acid formation by seeds of)
IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(formation of, by plant tissues, species specificity in)
IT Michaelis constant

(of [acyl carrier protein] acetyltransferase, of spinach)
IT Proteins
RL: BIOL (Biological study)
(acyl-carrier, acyl derivs., as primers in reconstituted fatty acid synthetase system of spinach)
IT **9077-10-5**
RL: BIOL (Biological study)
(I and II, in plants, activity levels of)
IT 57-10-3, biological studies 57-11-4, biological studies 143-07-7, biological studies 334-48-5 544-63-8, biological studies
RL: FORM (Formation, nonpreparative)
(formation of, by plant tissues, species specificity in)
IT **37237-39-1 37250-34-3 37251-08-4**
37257-17-3
RL: BIOL (Biological study)
(in plants, activity levels of)
IT 9045-77-6
RL: BIOL (Biological study)
(in plants, activity levels of components of)
IT **37257-16-2P**
RL: PREP (Preparation)
(of spinach, purification and function of)
IT **72-89-9** 2140-48-9 5060-32-2
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with [acyl carrier protein] acetyltransferase of spinach, kinetics of)
IT **9077-10-5**
RL: BIOL (Biological study)
(I and II, in plants, activity levels of)
RN 9077-10-5 HCAPLUS
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **37237-39-1 37250-34-3 37251-08-4**
37257-17-3
RL: BIOL (Biological study)
(in plants, activity levels of)
RN 37237-39-1 HCAPLUS
CN Dehydratase, 3-hydroxyacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37250-34-3 HCAPLUS
CN Reductase, 3-oxoacyl- [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37251-08-4 HCAPLUS
CN Reductase, enoyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

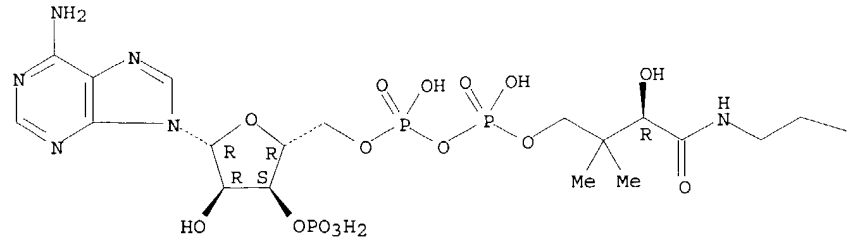
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37257-17-3 HCAPLUS
CN Malonyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **37257-16-2P**
RL: PREP (Preparation)
(of spinach, purification and function of)
RN 37257-16-2 HCAPLUS
CN Acetyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

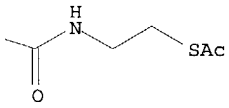
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **72-89-9**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with [acyl carrier protein] acetyltransferase of spinach, kinetics of)
RN 72-89-9 HCAPLUS
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



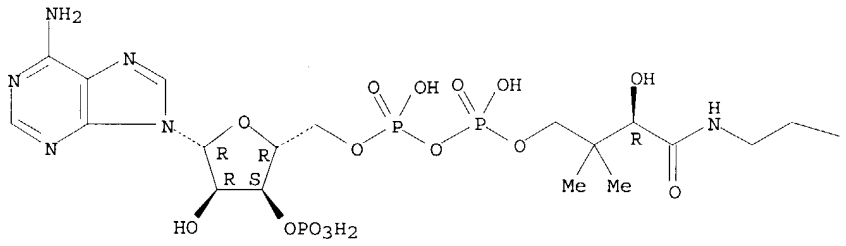
L84 ANSWER 21 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1982:594953 HCAPLUS
DN 97:194953
ED Entered STN: 12 May 1984
TI Isolation and function of spinach leaf **.beta.-ketoacyl -[acyl-carrier-protein] synthases**
AU Shimakata, Takashi; Stumpf, Paul K.
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA
SO Proceedings of the National Academy of Sciences of the United States of America (**1982**), 79(19), 5808-12
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
CC 7-2 (Enzymes)
AB Crude spinach leaf extract readily forms the stearoyl derivative of acyl-carrier-protein (ACP) when acetyl-ACP and malonyl-ACP are incubated together. Palmitoyl-ACP is also elongated by malonyl-ACP to stearoyl-ACP. When .beta.-ketoacyl-ACP synthase (EC 2.3.1.41) is purified with decanoyl-ACP as the assay substrate, palmitoyl-ACP elongation activity is lost. When palmitoyl-ACP is the assay substrate, another protein is isolated that specifically elongates palmitoyl-ACP to .beta.-ketostearoyl-ACP but has no activity towards decanoyl-ACP. The 1st protein is designated .beta.-ketoacyl-ACP synthase I and participates in the conversion of acetyl-ACP to palmitoyl-ACP, whereas the 2nd protein is designated .beta.-ketoacyl-ACP synthase II, and its substrate specificity is highly restricted to myristoyl-ACP and palmitoyl-ACP. The purification of synthase II is described, and its activity is compared to synthase I. Reconstitution expts. with highly purified nonassocd. enzymes in fatty acid synthesis plus synthases I and II clearly demonstrate the roles of these 2 proteins in fatty acid synthesis.
ST **ketoacyl acyl carrier protein synthase** spinach; leaf **ketoacyl acyl carrier protein synthase**
IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(formation of, by spinach leaf, **ketoacyl-[acyl carrier protein] synthase** multiform specificity in)
IT Spinach
(**ketoacyl-[acyl carrier protein] synthase** I and II of)
IT Leaf
(**ketoacyl-[acyl carrier protein] synthase** I and II of, of spinach)
IT Michaelis constant
(of **ketoacyl-[acyl carrier protein] synthase**)

IT Proteins
RL: BIOL (Biological study)
(acyl-carrier, acyl derivs., reaction of, with **ketoacyl-[acyl carrier protein] synthase**, kinetics of)
IT **9077-10-5P**
RL: PREP (Preparation)
(I and II, of spinach leaf, purification and specificity of)
IT **524-14-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with **ketoacyl-[acyl carrier protein] synthase**, kinetics of)
IT **9077-10-5P**
RL: PREP (Preparation)
(I and II, of spinach leaf, purification and specificity of)
RN 9077-10-5 HCAPLUS
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

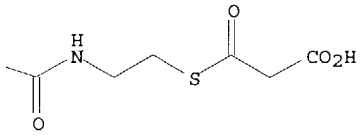
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **524-14-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with **ketoacyl-[acyl carrier protein] synthase**, kinetics of)
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



L84 ANSWER 22 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1982:522701 HCAPLUS
DN 97:122701
ED Entered STN: 12 May 1984
TI Partial separation of individual enzyme activities of an ACP-dependent fatty acid synthetase from barley chloroplasts
AU Hoej, Peter Bordier; Mikkelsen, Joern Dalgaard
CS Dep. Physiol., Carlsberg Lab., Copenhagen, DK-2500, Den.
SO Carlsberg Research Communications (**1982**), 47(2), 119-41
CODEN: CRCODS; ISSN: 0105-1938
DT Journal
LA English
CC 7-2 (Enzymes)
AB An acyl-carrier protein (ACP)-dependent fatty acid synthetase (fas) from barley chloroplast stroma was purified 5-fold by (NH4)2SO4 precipitation and gel filtration on Sephacryl S-300. The .beta.-ketoacyl-ACP reductase, .beta.-ketoacyl-ACP synthetase, acetyl-CoA:ACP transacylase, and malonyl-CoA:ACP transacylase activities were resolved on Sephacryl S-300 with apparent mol. wts. of 125, 92, 82, and 41 kilodaltons, resp. The fas activity exhibited an apparent mol. weight of 87 kilodaltons resulting from

the overlapping portions of the component activities. A 5th component of the active fas, ACP, was separated completely from the other 4 individual enzyme activities by (NH4)2SO4 precipitation When the fas purified by gel filtration was applied to a Matrex Gel Blue B column, the component activities were separated into 2 groups. A bound fraction contained all the malonyl-CoA:ACP transacylase, whereas the .beta.-ketoacyl synthetase activity was exclusively present in the nonbound fraction. Neither the bound nor the nonbound fraction showed any fas activity alone, but complete reconstitution of fas activity was obtained when both protein fractions were combined. The barley chloroplast fas is therefore not a multifunctional protein but consists of .gtoreq.5 sep. components. The fas required ACP, acetyl-CoA, malonyl-CoA, and NADH and NADPH (in concert) for activity.

ST fatty acid synthetase chloroplast barley

IT Barley
(fatty acid synthetase of chloroplast of, unifunctional enzymes of)

IT Chloroplast
(fatty acid synthetase of, unifunctional enzymes of)

IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(formation of, by fatty acid synthetase of chloroplast, regulation of)

IT Proteins
RL: BIOL (Biological study)
(acyl-carrier, fatty acid synthetase of chloroplast requirement for)

IT Enzymes
RL: PREP (Preparation)
(fatty acid-forming, unifunctional, of fatty acid synthetase of chloroplast, purification and properties of)

IT 53-57-6 58-68-4 **72-89-9 524-14-1**
RL: BIOL (Biological study)
(fatty acid synthetase of chloroplast requirement for)

IT 15502-74-6
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(fatty acid synthetase of chloroplast response to)

IT 9045-77-6P
RL: PREP (Preparation)
(of chloroplast, of barley, purification and properties of unifunctional enzymes of)

IT **9077-10-5P 37250-34-3P 37257-16-2P 37257-17-3P**
RL: PREP (Preparation)
(unifunctional, of fatty acid synthetase of chloroplast, purification and properties of)

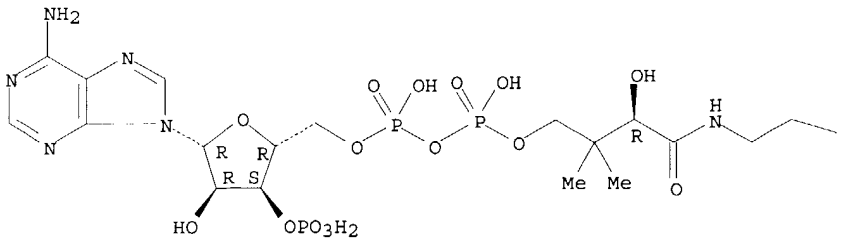
IT **72-89-9 524-14-1**
RL: BIOL (Biological study)
(fatty acid synthetase of chloroplast requirement for)

RN 72-89-9 HCAPLUS

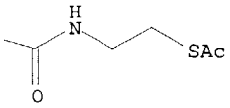
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



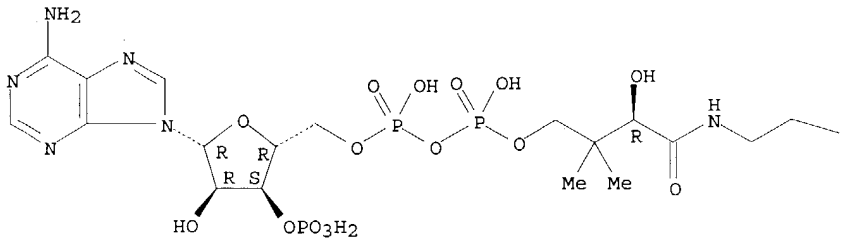
PAGE 1-B



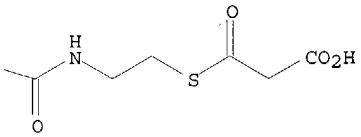
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IT **9077-10-5P 37250-34-3P 37257-16-2P**
37257-17-3P
RL: PREP (Preparation)
(unifunctional, of fatty acid synthetase of chloroplast, purification and properties of)
RN 9077-10-5 HCAPLUS
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37250-34-3 HCAPLUS
CN Reductase, 3-oxoacyl- [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37257-16-2 HCAPLUS
CN Acetyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37257-17-3 HCAPLUS
CN Malonyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

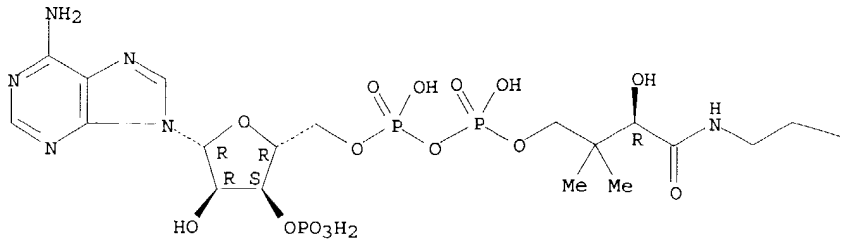
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 23 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1981:582875 HCAPLUS
DN 95:182875
ED Entered STN: 12 May 1984
TI Fatty acid synthetase from the Harderian gland of guinea pig: biosynthesis of methyl-branched fatty acids
AU Seyama, Yousuke; Otsuka, Hideaki; Kawaguchi, Akihiko; Yamakawa, Tamio
CS Fac. Med., Univ. Tokyo, Tokyo, 113, Japan
SO Journal of Biochemistry (Tokyo, Japan) (**1981**), 90(3), 789-97

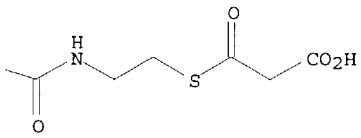
CODEN: JOBIAO; ISSN: 0021-924X
DT Journal
LA English
CC 7-2 (Enzymes)
Section cross-reference(s): 13
AB Fatty acid synthetase (I) was isolated from guinea pig Harderian gland. This enzyme complex differed from the I of the liver of the same animal. The former enzyme produced many odd-numbered and Me-branched fatty acids in the presence of methylmalonyl-CoA. These fatty acids are characteristic components of the lipid secreted by this gland. The chemical structure of this lipid has been identified as 1-O-alkyl-2,3-diacylglycerol by previous work from this laboratory The apparent Km values (5 .times. 10-6M) for acetyl-CoA and propionyl-CoA were the same, but the Vmax for propionyl-CoA was much higher than that for acetyl-CoA. The isoelec. point of I from Harderian gland was 5.3, and the mol. weight of the enzyme was 9 .times. 105 daltons. The .beta.-ketoacyl reductase had pro-S stereospecificity and the enoyl reductase had pro-R stereospecificity for NADPH.
ST fatty acid synthetase Harderian gland; methyl branched fatty acid formation
IT **Fatty acids, biological studies**
RL: BIOL (Biological study)
(methyl-branched, formation of, by fatty acid synthetase of Harderian gland)
IT Michaelis constant
(of fatty acid synthetase)
IT Lacrimal gland
(Harder's, fatty acid synthetase of, methyl-branched fatty acid formation by)
IT 53-57-6
RL: BIOL (Biological study)
(fatty acid synthetase component enzyme stereospecificity for)
IT 5502-94-3 5918-29-6 17670-87-0 53696-17-6 53696-23-4 53696-25-6 53696-26-7 63060-52-6 70641-72-4 79553-35-8 79553-36-9 79553-37-0
RL: FORM (Formation, nonpreparative)
(formation of, by fatty acid synthetase of Harderian gland)
IT 9045-77-6
RL: BIOL (Biological study)
(of Harderian gland, purification of and methyl-branched fatty acid formation by)
IT 79553-38-1P
RL: SPN (Synthetic preparation); PREP (Preparation)
(preparation of)
IT 1264-45-5
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with fatty acid synthetase, in presence of malonyl-CoA, methyl-branched fatty acid formation in)
IT **524-14-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with fatty acid synthetase, in presence of methylmalonyl-CoA, methyl-branched fatty acid formation in)
IT **72-89-9** 317-66-8
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with fatty acid synthetase, kinetics of)
IT **37250-34-3 37251-09-5**
RL: PRP (Properties)
(stereospecificity of, of Harderian gland, for NADPH)
IT **524-14-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with fatty acid synthetase, in presence of methylmalonyl-CoA, methyl-branched fatty acid formation in)
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



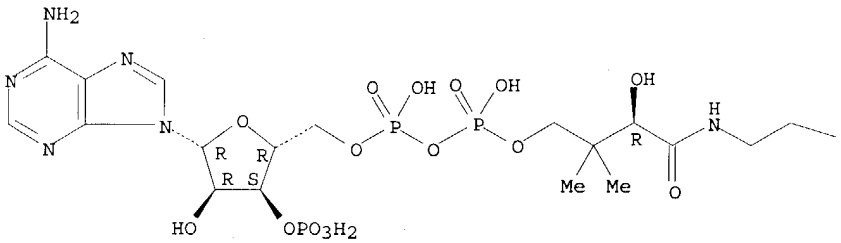
PAGE 1-B



IT **72-89-9**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with fatty acid synthetase, kinetics of)
RN 72-89-9 HCAPLUS
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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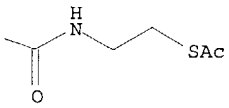


IT **37250-34-3 37251-09-5**
RL: PRP (Properties)
(stereospecificity of, of Harderian gland, for NADPH)
RN 37250-34-3 HCAPLUS
CN Reductase, 3-oxoacyl- [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37251-09-5 HCAPLUS
CN Reductase, enoyl-[acyl carrier protein] (reduced nicotinamide adenine dinucleotide phosphate) (9CI) (CA INDEX NAME)

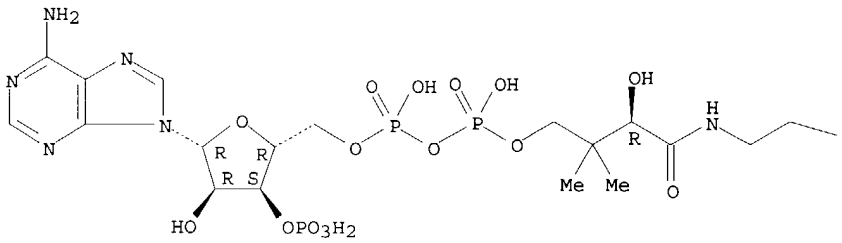
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L84 ANSWER 24 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1979:554995 HCAPLUS
DN 91:154995
ED Entered STN: 12 May 1984
TI In support of the roles of **malonyl-CoA** and carnitine **acyltransferase** I in the regulation of hepatic fatty acid oxidation and ketogenesis
AU McGarry, J. Denis; Foster, Daniel W.
CS Health Sci. Cent., Univ. Texas, Dallas, TX, 75235, USA
SO Journal of Biological Chemistry (**1979**), 254(17), 8163-8
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
CC 13-2 (Mammalian Biochemistry)
AB The rate of fatty acid synthesis in hepatocytes from meal-fed rats was manipulated over a wide range using glucose, lactate, and pyruvate to drive the system maximally and glucagon, 5-(tetradecyloxy)-2-furoic acid (I), or a combination of both agents to inhibit lipogenesis. Measurements were made of cellular malonyl CoA levels, long-chain acylcarnitine concentration and oleate-1-14C oxidation to total acid-soluble products, ketone bodies, and CO2. Regardless of the intervention employed, the rate of fatty acid synthesis correlated pos. with the tissue malonyl CoA concentration; both of these parameters were inversely related to the concentration of long-chain acylcarnitine which, in turn, was directly proportional to the rate of fatty acid oxidation Addition of glucagon, I, and carnitine to hepatocytes from meal-fed rats abolished the synthesis of malonyl CoA, stopped lipogenesis and stimulated fatty acid oxidation and ketogenesis to rates equivalent to those seen in hepatocytes from fasted animals. The data provide further support for the central roles of malonyl CoA and carnitine acyltransferase I in the coordination of hepatic fatty acid synthesis and oxidation They also establish that the changes in fatty acid oxidation and ketogenesis produced by fasting can be entirely accounted for by removal of the malonyl CoA-mediated inhibition of carnitine acyltransferase I activity, coupled with a rise in hepatic carnitine content.
ST liver fatty acid metab regulation; hepatocyte fatty acid metab regulation; malonyl CoA hepatocyte fatty acid; carnitine acyltransferase hepatocyte fatty acid
IT Glycolysis
(by hepatocytes, fatty acid metabolism in relation to)
IT Inanition
(fatty acid metabolism by hepatocytes in, carnitine **acyltransferase** I and **malonyl CoA** in)
IT Ketone body
RL: FORM (Formation, nonpreparative)
(formation of, by hepatocytes, carnitine **acyltransferase** I and **malonyl CoA** in)
IT **Fatty acids, biological studies**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by hepatocytes, carnitine **acyltransferase** I and **malonyl CoA** in)
IT Liver, metabolism
(hepatocyte, fatty acid metabolism by, carnitine and **acyltransferase** I and **malonyl CoA** in)
IT 39386-49-7
RL: BIOL (Biological study)
(I, in fatty acid metabolism by hepatocyte)
IT 541-15-1 9007-92-5, biological studies 54857-86-2
RL: BIOL (Biological study)
(fatty acid metabolism by hepatocyte in response to)
IT 541-15-1D, long-chain acyl derivs.
RL: BIOL (Biological study)
(fatty acid metabolism by hepatocytes in relation to)
IT 127-17-3, biological studies
RL: BIOL (Biological study)
(fatty acid metabolism by hepatocytes in response to glucose and lactate and)
IT 50-21-5, biological studies
RL: BIOL (Biological study)
(fatty acid metabolism by hepatocytes in response to glucose and pyruvate and)
IT 50-99-7, biological studies
RL: BIOL (Biological study)
(fatty acid metabolism by hepatocytes in response to lactate and pyruvate and)
IT **524-14-1**

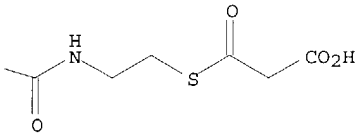
RL: BIOL (Biological study)
(in fatty acid metabolism by hepatocyte)
IT 112-80-1, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by hepatocytes, carnitine **acyltransferase** I and **malonyl CoA** in)
IT **524-14-1**
RL: BIOL (Biological study)
(in fatty acid metabolism by hepatocyte)
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



L84 ANSWER 25 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1977:465524 HCAPLUS
DN 87:65524
ED Entered STN: 12 May 1984
TI 2-Methylacetoacetate reductase and possible propionyl coenzyme A **condensing enzyme** activity in branched chain volatile fatty acid synthesis by Ascaris lumbricoides
AU Suarez de Mata, Zadila; Saz, Howard J.; Pasto, Daniel J.
CS Dep. Biol., Univ. Notre Dame, Notre Dame, IN, USA
SO Journal of Biological Chemistry (**1977**), 252(12), 4215-24
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
CC 12-1 (Nonmammalian Biochemistry)
Section cross-reference(s): 7
AB A. lumbricoides ferments carbohydrate to a mixture of end products, principally 2-methylbutyrate and 2-methylvalerate. Propionyl CoA may be the direct precursor of the branched-chain volatile acids by a path similar to a reverse of the .beta.-oxidation path. Neither fatty acid synthetase nor enoyl CoA reductase activities were demonstrable in Ascaris muscle prepns. Two new enzymes were partially purified and characterized from Ascaris mitochondria: NADH-linked 2-methylacetoacetate reductase and NADH-linked propionyl CoA reductase (propionyl CoA condensing enzyme). The 2-methylacetoacetate reductase was unique in that the apparent CoA ester requirement was substituted for by the Et ester of, e.g., 2-methylacetoacetate or 2-methylpropioacetate (possible precursors for 2-methylbutyrate and 2-methylvalerate, resp.). The product of the enzymic reduction of Et methylacetoacetate was an erythro isomer of Et 3-hydroxymethylbutyrate. Propionyl CoA condensing enzyme activity was >10-fold more active with propionyl CoA than with acetyl CoA as substrate. The product of the coupled propionyl CoA condensation and reductase reactions was tentatively identified as 3-hydroxy-2-methylvaleryl CoA.
ST fatty acid branched metab Ascaris; methylacetoacetate reductase nematode;

propionyl CoA reductase Ascaris

IT Muscle, metabolism
(branched-chain fatty acid formation by mitochondria of, of ascarid, methylacetoacetate reductase and propionyl CoA reductase in relation to)

IT Ascaris suum
(branched-chain fatty acid formation by muscle mitochondria of, methylacetoacetate reductase and propionyl CoA reductase in relation to)

IT Mitochondria
(branched-chain fatty acid formation by, of muscle of ascarid, methylacetoacetate reductase and propionyl CoA reductase in relation to)

IT Michaelis constant
(of methylacetoacetate reductase)

IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(branched-chain, formation of, by muscle mitochondria of ascarid, methylacetoacetate reductase and propionyl CoA reductase in relation to)

IT 51898-35-2 64051-74-7
RL: FORM (Formation, nonpreparative)
(formation of, by muscle mitochondria of ascarid)

IT 9027-13-8 9028-41-5
RL: BIOL (Biological study)
(of muscle mitochondria, of ascarid)

IT 63774-52-7 63774-53-8
RL: BIOL (Biological study)
(of muscle mitochondria, of ascarid, branched fatty acid formation in relation to)

IT 609-14-3 759-66-0 1264-45-5 1420-36-6 16508-89-7 27372-03-8 40309-41-9
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with methylacetoacetate reductase of muscle mitochondria of ascarid)

IT **72-89-9** 317-66-8 **524-14-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with propionyl CoA reductase of muscle mitochondria of ascarid)

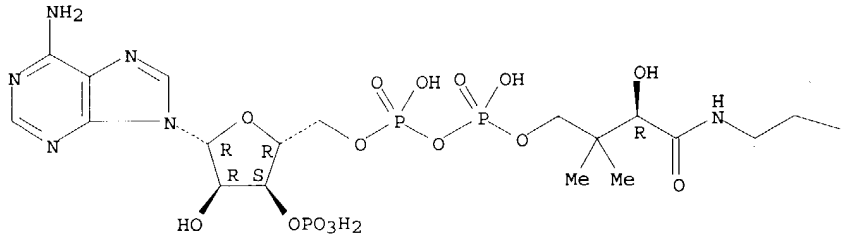
IT **72-89-9 524-14-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with propionyl CoA reductase of muscle mitochondria of ascarid)

RN 72-89-9 HCAPLUS

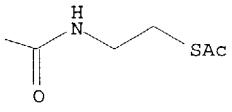
CN Coenzyme A, S-acetate (6CI, 8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B

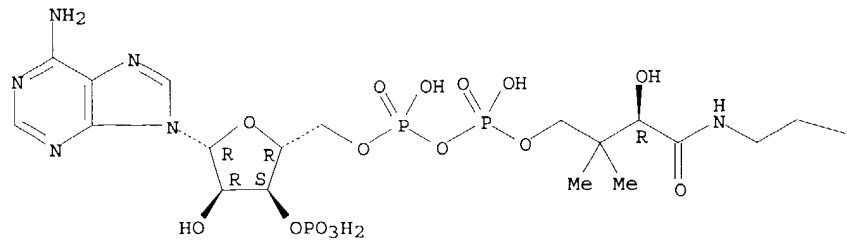


RN 524-14-1 HCAPLUS

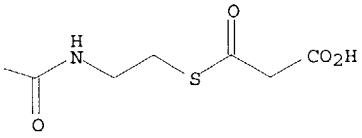
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



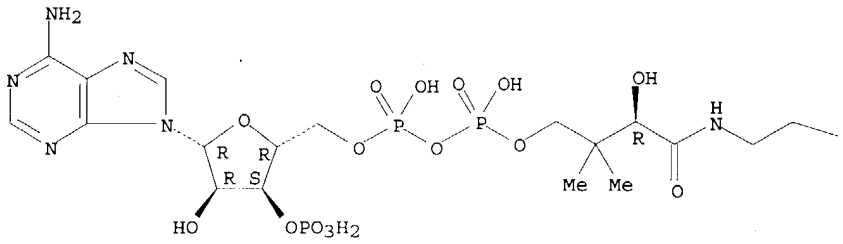
L84 ANSWER 26 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1975:94762 HCAPLUS
DN 82:94762
ED Entered STN: 12 May 1984
TI Mechanism and control of the malonyl-CoA-dependent chain elongation of fatty acids. Malonyl transfer reaction
AU Podack, Eckhard R.; Saathoff, Gisela; Seubert, Werner
CS Physiol.-Chem. Inst., Univ. Goettingen, Goettingen, Fed. Rep. Ger.
SO European Journal of Biochemistry (**1974**), 50(1), 237-43
CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
CC 7-4 (Enzymes)
AB The enoyl CoA reductase activity of the purified microsomal chain elongation system of rat liver was inhibited noncompetitively by long-chain acyl CoA and competitively by malonyl CoA. The multienzyme complex catalyzed the transfer of the malonyl residue from malonyl CoA to pantetheine and CoASH with high affinities for the physiol. acceptor and donator CoASH (Km = 20 .mu.M) and malonyl CoA (Km = 22 .mu.M), resp. The malonyl transfer was competitively inhibited by octanoyl CoA, 2,3-trans-octenoyl CoA, and 3-oxooctanoyl CoA. A common transferase catalyzing the exchange of the acyl moieties of malonyl enzyme and of the various enzyme-bound intermediates of chain elongation with free CoA was thus assumed. Observations (Nugteren, D.H., 1965) suggesting a microsomal chain elongation at the level of the CoA derivatives were explained by a rapid exchange of enzyme-bound intermediates of the chain elongation process with free CoASH.
ST fatty acid chain elongation; enoyl CoA reductase liver; **malonyl transferase** liver microsome
IT **Fatty acids, biological studies**
RL: BIOL (Biological study)
(chain elongation of, by liver microsome, **malonyl transferase** in relation to)
IT Liver, metabolism
(fatty acid chain elongation and malonyl transfer by)
IT Microsome
(**malonyl transferase** of, of liver, mechanism of)
IT Kinetics, enzymic
(of **malonyl transferase**)
IT 37251-07-3
RL: BIOL (Biological study)
(of liver microsome, malonyl transfer mechanism in relation to)
IT **37257-17-3**
RL: PROC (Process)

(of liver microsome, mechanism of)
IT **85-61-0**, reactions 496-65-1 **524-14-1** 1264-52-4
6157-84-2 10018-94-7 54684-64-9
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with **malonyl transferase**, kinetics of)
IT **37257-17-3**
RL: PROC (Process)
(of liver microsome, mechanism of)
RN 37257-17-3 HCAPLUS
CN Malonyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

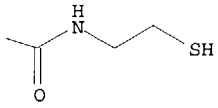
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **85-61-0**, reactions **524-14-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with **malonyl transferase**, kinetics of)
RN 85-61-0 HCAPLUS
CN Coenzyme A (8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



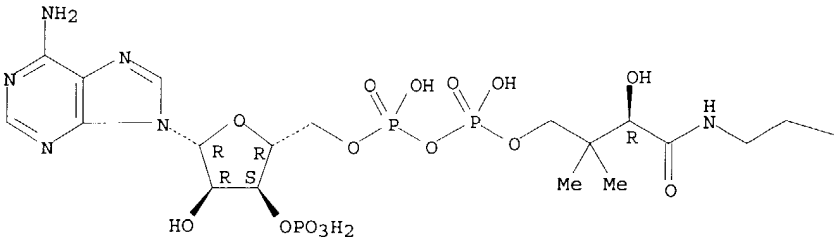
PAGE 1-B



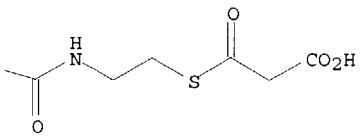
RN 524-14-1 HCAPLUS
CN Coenzyme A, S-(hydrogen propanedioate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



=> d all hitstr l67 tot

L67 ANSWER 1 OF 6 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:489673 HCAPLUS
DN 135:87150
ED Entered STN: 06 Jul 2001
TI High throughput screen for inhibitors of fatty acid biosynthesis in bacteria
IN Murphy, Christopher; Youngman, Philip
PA Millennium Pharmaceuticals Inc., USA
SO PCT Int. Appl., 34 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-68
ICS A61K031-00; A61P031-04
CC 1-5 (Pharmacology)
Section cross-reference(s): 3, 10
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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	WO 2001048248	A3	20020919		
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	US 6656703	B1	20031202	US 1999-474140	19991229 <--
PRAI	US 1999-474140	A1	19991229 <--		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2001048248	ICM	C12Q001-68
	ICS	A61K031-00; A61P031-04
US 6656703	ECLA	C12Q001/68P <--

AB Methods for identifying compds. that are inhibitors of bacterial fatty acid biosynthesis are disclosed. Such compds. can be used as lead compds. in methods for preparing antibacterial agents for treating bacterial infections (e.g., in humans, animals, and plants). Inhibitors of bacterial fatty acid synthesis can also be tested for their ability to inhibit synthesis of acylated homoserine lactones. Compds. that inhibit synthesis of acylated homoserine lactones can be used as inhibitors of bacterial virulence. The disclosed methods allow for high throughput screening of libraries of test compds.
ST drug screening fatty acid synthesis inhibitor bacteria; antibacterial agent screening fatty acid synthesis inhibitor
IT Promoter (genetic element)
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(PyhfB; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)
IT Promoter (genetic element)
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(PylpC; high throughput screen for inhibitors of fatty acid

biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Phospholipids, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(acetate incorporation into; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Infection
(bacterial; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Gene, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(cat; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Immunoassay
(for reporter gene product; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Gene, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(green fluorescent protein-encoding; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Proteins, specific or class
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(green fluorescent, gene encoding; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Antibacterial agents
DNA sequences
Drug delivery systems
Drug screening
(high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Promoter (genetic element)
Reporter gene
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT **Fatty acids, biological studies**
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(high throughput screen for inhibitors of fatty acid **biosynthesis** in bacteria which stimulate gene promoter linked to reporter gene)

IT Gene, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(lacZ; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Gene, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(luciferase-encoding; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Antibodies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(to reporter gene product; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Streptococcus
(treatment of endocarditis from infection by; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Enterococcus faecium
Granulicatella adiacens
Streptococcus agalactiae

Streptococcus pneumoniae
Streptococcus pyogenes
Streptococcus sanguinis
(treatment of infection from; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT Gene, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(uidA; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT 3380-34-5, Triclosan 17397-89-6, Cerulenin
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antibacterial activity of; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT 64-19-7, Acetic acid, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(determination of fatty acid incorporation of; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT **37251-08-4, Enoyl-acyl carrier protein reductase**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(determination of inhibition of; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT 1192-20-7D, Homoserine lactone, acylated
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(determination of synthesis of; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT 9014-00-0, Luciferase 9040-07-7, Chloramphenicol transacetylase
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(gene encoding; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT 349517-60-8 349517-61-9 349517-62-0 349517-63-1
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(nucleotide sequence; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

IT 349527-22-6 349527-23-7 349527-24-8 349527-25-9 349527-26-0
349527-27-1 349527-28-2 349527-29-3
RL: PRP (Properties)
(unclaimed nucleotide sequence; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria)

IT **37251-08-4, Enoyl-acyl carrier protein reductase**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(determination of inhibition of; high throughput screen for inhibitors of fatty acid biosynthesis in bacteria which stimulate gene promoter linked to reporter gene)

RN 37251-08-4 HCAPLUS
CN Reductase, enoyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L67 ANSWER 2 OF 6 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:742235 HCAPLUS
DN 133:291952
ED Entered STN: 20 Oct 2000
TI Modification of lipid biosynthesis by DNA shuffling
IN Yuan, Ling; Raillard, Sun Ai; Lassner, Michael
PA Maxygen, Inc., USA
SO PCT Int. Appl., 90 pp.

CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N015-10
ICS C12N015-82; A01H005-00
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 7, 11
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000061740	A1	20001019	WO 2000-US9285	20000406 <--

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-128707P P 19990410 <--
CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2000061740	ICM	C12N015-10
	ICS	C12N015-82; A01H005-00

AB Methods of modulating lipid production in cells and whole organisms by DNA shuffling are provided. Single genes, operons, lipid biosynthetic cycles and whole genomes can be recombined to produce cells and organisms with desirable lipid synthetic or metabolic activity. Libraries of recombined lipid synthetic nucleic acids and organisms are also provided. Modification of lipid saturation, fatty acid composition, fatty alc. composition, wax composition, acyl chain length, location of fatty acid accumulation, triglyceride yield, substrate specificity, expression level, are described. A decrease in susceptibility to protease cleavage, high or low pH levels, extreme temps., are also claimed. A decrease in toxicity, and modification of methyltransferase activity resulting in formation of branched chain, cyclopropyl, methoxy, or keto fatty acids, are also described. Use of two-hybrid system in detecting the changes in lipid biosynthetic activity is also claimed. Screening of libraries, such as phage display library is described. Crop plants such as corn, peanut, barley, millet, rice, soybean, sorghum, wheat, oats, sunflower, or nut whose lipid biosynthetic activity modified, are claimed. DNA shuffling is a powerful process for directed evolution, which generates diversity by recombination, combining useful mutations from individual genes.

ST lipid biosynthesis modification plant DNA shuffling
IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(ACP (acyl-carrier), 3-hydroxy acyl; modification of lipid biosynthesis by DNA shuffling)
IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(ACP (acyl-carrier); modification of lipid biosynthesis by DNA shuffling)
IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(DNA-binding; modification of lipid biosynthesis by DNA shuffling)
IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(FABP (fatty acid-binding protein); modification of lipid biosynthesis by DNA shuffling)
IT Genetic element
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(Lox, protein; modification of lipid biosynthesis by DNA shuffling)
IT Operon
(PKS-like; modification of lipid biosynthesis by DNA shuffling)
IT **Fatty acids, biological studies**
Waxes
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)

(composition, modification of; modification of lipid **biosynthesis** by DNA shuffling)
IT Protein degradation
(decrease in susceptibility to; modification of lipid biosynthesis by DNA shuffling)
IT Cytotoxicity
(decrease in; modification of lipid biosynthesis by DNA shuffling)
IT Alcohols, biological studies
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(fatty, composition, modification of; modification of lipid biosynthesis by DNA shuffling)
IT Recombination, genetic
(gene shuffling; modification of lipid biosynthesis by DNA shuffling)
IT pH
(high or low, stability against; modification of lipid biosynthesis by DNA shuffling)
IT Cyanobacteria
Escherichia coli
Pseudomonas putida
Synechocystis
(library; modification of lipid biosynthesis by DNA shuffling)
IT Operon
(lux; modification of lipid biosynthesis by DNA shuffling)
IT Algae
Animal
Bacteria (Eubacteria)
Fungi
Genetic engineering
Phage display library
Plant (Embryophyta)
Thermal stability
(modification of lipid biosynthesis by DNA shuffling)
IT **Lipids**, biological studies
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(modification of lipid **biosynthesis** by DNA shuffling)
IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(oleosins; modification of lipid biosynthesis by DNA shuffling)
IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(phospholipid-exchanging, phosphatidylcholine; modification of lipid biosynthesis by DNA shuffling)
IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(sulfolipid biosynthesis; modification of lipid biosynthesis by DNA shuffling)
IT Barley
Compositae (Asteraceae)
Corn
Crop (plant)
Grass (Poaceae)
Legume (Fabaceae)
Millet
Oat
Peanut (Arachis hypogaea)
Rice (Oryza sativa)
Sorghum
Soybean (Glycine max)
Sunflower
Wheat
(transgenic; modification of lipid biosynthesis by DNA shuffling)
IT Genetic methods
(two-hybrid screening; modification of lipid biosynthesis by DNA shuffling)
IT **Fatty acids, biological studies**
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(unsatd.; modification of lipid **biosynthesis** by DNA

shuffling)
IT Glycerides, biological studies
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(yield; modification of lipid biosynthesis by DNA shuffling)
IT Oxidation
(.beta.-, enzyme for; modification of lipid biosynthesis by DNA shuffling)
IT 9067-83-8P, CDP-diacylglycerol synthase
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(ER; modification of lipid biosynthesis by DNA shuffling)
IT 9025-77-8P, Phosphatidic acid phosphatase 9033-46-9P, Phosphatidylglycerol phosphatase 9068-49-9P, Phosphatidylglycero-phosphate synthase 9082-66-0P, Linoleate desaturase 72536-70-0P, Oleate desaturase
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(Plastidial and ER; modification of lipid biosynthesis by DNA shuffling)
IT 9001-62-1P, Lipase 9001-86-9P, Phospholipase C 9001-87-0P, Phospholipase D 9013-18-7P, Long-chain acyl-CoA synthetase 9023-93-2P, Acetyl CoA carboxylase 9026-13-5P, Diacylglycerol choline phosphotransferase 9026-34-0P, Cholinephosphate cytidylyltransferase 9026-67-9P, Choline kinase 9027-01-4P 9028-40-4P, **.beta.-Ketoacyl reductase** 9029-60-1P, Lipoxygenase 9029-96-3P, Glycerol-3-phosphate acyltransferase 9031-56-5P, Ligase 9033-25-4P, Methyltransferase 9037-80-3P, Reductase 9054-78-8P, Phosphatidylserine decarboxylase **9077-10-5P**, **.beta.-Ketoacyl-ACP synthase 37250-34-3P**, **.beta.-Ketoacyl-ACP reductase 37251-08-4P**, **Enoyl-ACP reductase 37256-86-3P**, Stearoyl-ACP desaturase **37257-17-3P**, **Malonyl-CoA transacylase** 37277-55-7P, Monogalactosyldiacyl-glycerol synthase 51845-48-8P, Cyclopropane fatty acid synthase 51901-16-7P 58943-36-5P, Thioesterase 60382-71-0P, Diacylglycerol kinase **68009-83-6P**, Acyl-ACP thioesterase 69403-06-1P, Fatty acid Elongase 69913-00-4P, UDP-galactose:diacylgalactosylglycerol galactosyltransferase 71833-11-9P, Hydroperoxide lyase **77322-37-3P**, Acyl-acyl carrier protein synthase 88414-92-0P 94219-29-1P, Fatty acid Elongase 103843-28-3P, Desaturase 115926-52-8P, Phosphatidylinositol-3-kinase 159202-88-7P, Cis-trans-Fatty acid isomerase 300669-15-2P, Palmitoylphosphatidylglycerol desaturase 300676-64-6P, Monogalactosyldiacylglycerol palmitoyl-specific desaturase
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(modification of lipid biosynthesis by DNA shuffling)
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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(2) Cahoon, E; PNAS U S A 1997, V94, P4872 HCAPLUS
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(10) Schmidt-Dannert, C; TRENDS IN BIOTECHNOLOGY 1999, V17(4), P135 HCAPLUS
(11) Stemmer, W; PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA 1994, V91, P10747 HCAPLUS
(12) Studiengesellschaft Kohle Mbh; DE 19731990 A 1999 HCAPLUS
IT **9077-10-5P**, **.beta.-Ketoacyl-ACP synthase 37250-34-3P**, **.beta.-Ketoacyl -ACP reductase 37251-08-4P**, **Enoyl-ACP reductase 37256-86-3P**, Stearoyl-ACP desaturase **37257-17-3P**, **Malonyl-CoA transacylase 68009-83-6P**, Acyl-ACP thioesterase **77322-37-3P**, Acyl-acyl carrier protein synthase
RL: BPN (Biosynthetic preparation); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(modification of lipid biosynthesis by DNA shuffling)
RN 9077-10-5 HCAPLUS
CN Synthase, 3-oxoacyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37250-34-3 HCAPLUS
CN Reductase, 3-oxoacyl- [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37251-08-4 HCAPLUS
CN Reductase, enoyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37256-86-3 HCAPLUS
CN Desaturase, acyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 37257-17-3 HCAPLUS
CN Malonyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 68009-83-6 HCAPLUS
CN Hydrolase, acyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 77322-37-3 HCAPLUS
CN Acyltransferase, [acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L67 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:291289 HCAPLUS
DN 132:318601
ED Entered STN: 05 May 2000
TI Use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.
IN Dunham, Steven Alan; Olson, Eric
PA Warner-Lambert Company, USA
SO PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-68
ICS C07K014-22; C07K014-245; C12R001-19; C12R001-36; C12N015-10; C12Q001-18
CC 3-2 (Biochemical Genetics)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2000024932	A1	20000504	WO 1999-US22118	19990923	<--
	W: AE, AL, AU, BA, BB, BG, BR, CA, CN, CR, CU, CZ, DM, EE, GD, GE, HR, HU, ID, IL, IN, IS, JP, KP, KR, LC, LK, LR, LT, LV, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, SL, TR, TT, TZ, UA, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	CA 2343318	AA	20000504	CA 1999-2343318	19990923	<--
	AU 9961607	A1	20000515	AU 1999-61607	19990923	<--
	BR 9914844	A	20010710	BR 1999-14844	19990923	<--
	TR 200101142	T2	20010821	TR 2001-200101142	19990923	<--
	EP 1124988	A1	20010822	EP 1999-948428	19990923	<--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO					
	JP 2002528094	T2	20020903	JP 2000-578484	19990923	<--
PRAI	US 1998-105965P	P	19981028	<--		
	WO 1999-US22118	W	19990923	<--		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2000024932	ICM	C12Q001-68
	ICS	C07K014-22; C07K014-245; C12R001-19; C12R001-36; C12N015-10; C12Q001-18
WO 2000024932	ECLA	C07K014/22; C07K014/245; C12N015/10B; C12Q001/68D4; C12R001/19; C12R001/36 <--

AB A method of using long-range error-prone PCR to generate and identify mutations leading to a given phenotype are described. Regions of .apprx.10 kilobases of a genome covering .apprx.100 kb are amplified with error-prone PCR and are transformed in pools into the source organism and

transformants screened for the phenotype of interest, e.g. antibiotic resistance. The pool of amplification products is then fractionated to identify the fragment carrying the mutation and when a single amplification product is identified, it can be further analyzed to localize the mutation. Use of the method to generate quinolone-resistant mutants of the Neisseria gonorrhoeae hyrA gene is demonstrated.

ST error prone PCR antibiotic resistance generation characterization; fluoroquinolone resistance Neisseria generation error prone PCR; DNA gyrase antibiotic resistance error prone PCR

IT Enzymes, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(DNA gyrases, identifying antibiotic resistant mutants of; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT PCR (polymerase chain reaction)
(error-prone; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(fabI, mutagenesis of; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT **Drug screening**
(for antibiotics; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT Escherichia
Escherichia coli
Haemophilus
Haemophilus influenzae
Neisseria
Neisseria gonorrhoeae
Neisseria meningitidis
Staphylococcus
Staphylococcus aureus
Staphylococcus epidermidis
Streptococcus
Streptococcus pneumoniae
Streptococcus pyogenes
(generation of antibiotic resistance in; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT Antibiotic resistance
(generation of mutants for study of; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(generation of resistance to antibiotics inhibiting **biosynthesis** of; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gyrA, mutagenesis of; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT Mutagens
UV radiation
(in generation of resistance to antibiotics; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT Genetic mapping
(phys., of mutations; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT Antibiotics
(quinolone, generation of resistance to; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT Mutation
(use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT 13721-01-2D, derivs., antibiotics
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Quinolone antibiotics, generation of resistance to; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)

IT **37251-09-5** 80449-01-0, DNA topoisomerase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(generation of antibiotic resistant variants of; use of error-prone PCR

to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)
IT 1133-63-7D, [1,1'-Biphenyl]-2,3-diol, derivs., antibiotics 3380-34-5, Triclosan 85721-33-1, Ciprofloxacin 105956-97-6, Clinafloxacin
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(generation of resistance to; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)
IT 266992-07-8, 3: PN: WO0024932 SEQID: 4 unclaimed DNA 266992-08-9, 4: PN: WO0024932 SEQID: 5 unclaimed DNA 266992-09-0, 6: PN: WO0024932 SEQID: 7 unclaimed DNA 266992-10-3, 8: PN: WO0024932 SEQID: 9 unclaimed DNA 266992-11-4, 9: PN: WO0024932 SEQID: 10 unclaimed DNA 266992-12-5 266992-13-6 266992-14-7 266992-15-8
RL: PRP (Properties)
(unclaimed nucleotide sequence; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)
IT **260027-88-1** 266992-06-7
RL: PRP (Properties)
(unclaimed protein sequence; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)
IT 266676-10-2
RL: PRP (Properties)
(unclaimed sequence; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Bayer Ag; EP 0688873 A 1995 HCAPLUS
(2) Belland, R; MOLECULAR MICROBIOLOGY 1994, V14(2), P371 HCAPLUS
(3) Collins, D; US 5686590 A 1997 HCAPLUS
(4) Deguchi, T; ANTIMICROBIAL AGENTS AND CHEMOTHERAPY 1995, V39(2), P561 HCAPLUS
(5) Deguchi, T; ANTIMICROBIAL AGENTS AND CHEMOTHERAPY 1996, V40(4), P1020 HCAPLUS
(6) Heath, R; JOURNAL OF BIOLOGICAL CHEMISTRY 1998, V273(46), P30316 HCAPLUS
(7) Jones, D; BIOTECHNIQUES 1991, V10(1), P62 HCAPLUS
(8) Kok, R; JOURNAL OF BACTERIOLOGY 1997, V179(13), P4270 HCAPLUS
(9) Macek, K; FASEB JOURNAL 1999, V13(7Sup), PA1350
(10) McMurry, L; NATURE 1998, V394(394), P531
(11) Smithkline Beecham Corp; EP 0826774 A 1998 HCAPLUS
(12) Tanaka, M; THE JOURNAL OF UROLOGY 1998, V159, P2215 HCAPLUS
(13) Univ Temple; EP 0081078 A 1983 HCAPLUS
(14) Weigel, L; ANTIMICROBIAL AGENTS AND CHEMOTHERAPY 1998, V42(10), P2661 HCAPLUS
IT **37251-09-5**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(generation of antibiotic resistant variants of; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)
RN 37251-09-5 HCAPLUS
CN Reductase, enoyl-[acyl carrier protein] (reduced nicotinamide adenine dinucleotide phosphate) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **260027-88-1**
RL: PRP (Properties)
(unclaimed protein sequence; use of error-prone PCR to generate and identify point mutations within bacterial DNA gyrase and fabI genes.)
RN 260027-88-1 HCAPLUS
CN Enoyl-(acyl-carrier-protein) reductase (Neisseria meningitidis strain MD58 gene NMB0336) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L67 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:487416 HCAPLUS
DN 131:134684
ED Entered STN: 06 Aug 1999
TI **Enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening
IN Levy, Stuart B.; Mcmurry, Laura M.
PA Trustees of Tufts College, USA
SO PCT Int. Appl., 80 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-18
ICS G01N033-94; G01N033-68; C12N015-53; C12N009-02; C07K014-31;

C07K016-40; A61K038-43; C12Q001-68; G01N033-573
CC 63-7 (Pharmaceuticals)
Section cross-reference(s): 1, 10, 62
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9937800	A1	19990729	WO 1999-US1288	19990122 <--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2319115	AA	19990729	CA 1999-2319115	19990122 <--
	AU 9923324	A1	19990809	AU 1999-23324	19990122 <--
	EP 1049799	A1	20001108	EP 1999-903262	19990122 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2002510463	T2	20020409	JP 2000-528707	19990122 <--
	US 2004024068	A1	20040205	US 2003-377250	20030227 <--
PRAI	US 1998-72244P	P	19980123 <--		
	US 1998-13440	A	19980126 <--		
	US 1999-235896	B1	19990122 <--		
	WO 1999-US1288	W	19990122 <--		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 9937800	ICM	C12Q001-18
	ICS	G01N033-94; G01N033-68; C12N015-53; C12N009-02; C07K014-31; C07K016-40; A61K038-43; C12Q001-68; G01N033-573
US 2004024068	ECLA	C07K014/245; C12N009/02C; C12Q001/18 <--

AB Methods and mutants for identifying an antimicrobial compound which interacts with an ER (enoyl-ACP reductase) polypeptide are disclosed. In particular, the method pertains to screens for identifying an antimicrobial compound using FabI or InhA mutant cells or polypeptides.

ST antimicrobial screening **enoyl ACP reductase** binding sequence

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FabI, protein product; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT Proteins, specific or class
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(FabI; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(InhA, protein product; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT Proteins, specific or class
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(InhA; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT Enzyme functional sites
(NAD/NADP-binding cleft; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT **Fatty acids, biological studies**
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(**biosynthesis**; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT Soaps
RL: BUU (Biological use, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(containing bactericide; **enoyl**-ACP (**acyl**

carrier protein) **reductase**-interacting
substances in antimicrobial screening)
IT Biological transport
(efflux, pumps, inhibitors of; **enoyl**-ACP (**acyl**
carrier protein) **reductase**-interacting
substances in antimicrobial screening)
IT Transport proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(efflux-mediating AcrAB, inhibitors; **enoyl**-ACP (**acyl**
carrier protein) **reductase**-interacting
substances in antimicrobial screening)
IT Actinomyces
Antibiotic resistance
Antibiotics
Antimicrobial agents
Bioassay
Borrelia
Campylobacter
Candida
Dentifrices
Deodorants
Detergents
Disinfectants
Drug screening
Enterococcus
Erwinia
Escherichia
Fungi
Fungicides
Gram-negative bacteria
Gram-positive bacteria (Firmicutes)
Helicobacter
Klebsiella
Leptonema
Leptospira
Listeria
Mouthwashes
Mycobacterium
Mycobacterium smegmatis
Protein sequences
Protozoacides
Pseudomonas
Salmonella
Sarcina
Serratia
Shigella
Spirochaeta
Spirochaetales
Staphylococcus
Streptococcus
Treponema
Yersinia
cDNA sequences
(**enoyl**-ACP (**acyl carrier protein**
) **reductase**-interacting substances in antimicrobial
screening)
IT Antibodies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
(Biological study); PROC (Process)
(monoclonal; **enoyl**-ACP (**acyl carrier**
protein) **reductase**-interacting substances in
antimicrobial screening)
IT Mutation
(substitution, in ER polypeptides; **enoyl**-ACP (**acyl**
carrier protein) **reductase**-interacting
substances in antimicrobial screening)
IT **148998-18-9P**, Protein (Escherichia coli clone pHAP1 gene envM
reduced)
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BPR
(Biological process); BSU (Biological study, unclassified); PRP
(Properties); BIOL (Biological study); OCCU (Occurrence); PREP
(Preparation); PROC (Process)
(amino acid sequence; **enoyl**-ACP (**acyl**
carrier protein) **reductase**-interacting
substances in antimicrobial screening)
IT **37251-08-4**, **Enoyl-ACP reductase**

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(**enoyl-ACP (acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT 3380-34-5D, Triclosan, derivs.
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(**enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT 54-85-3, Isoniazid 536-33-4, Ethionamide 21508-48-5, 1,2,3-Diazaborine
RL: MSC (Miscellaneous)
(**enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT 72-18-4, Valine, biological studies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(glycine substituted by; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT 63-91-2, Phenylalanine, biological studies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(leucine substitution for; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT 72-19-5, Threonine, biological studies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(methionine substituted by; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT 61-90-5, Leucine, biological studies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(phenylalanine substituted by; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT 63-68-3, Methionine, biological studies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(threonine substitution for; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

IT 56-40-6, Glycine, biological studies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(valine substitution for; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Anon; 1996, 7, HCAPLUS
(2) Anon; 1997, 19, HCAPLUS
(3) Anon; MEDLINE
(4) Bergler, H; EURPEAN JOURNAL OF BIOCHEMISTRY 1996, V242(3), P689 HCAPLUS
(5) Blanchard, J; ANNUAL REVIEWS OF BIOCHEMISTRY 1996, V65, P215 HCAPLUS
(6) Industria E Comercio De Cosmeticos Natura Ltda; WO 9802139 A 1998 HCAPLUS
(7) Regos, J; DERMATOLOGICA 1979, V158(1), P72 MEDLINE
(8) Sacchettini, J; US 5702935 A 1997 HCAPLUS
(9) Sacchettini, J; US 5837480 A 1998 HCAPLUS
(10) Smithkline Beecham Corporation; EP 0826774 A 1998 HCAPLUS

IT **148998-18-9P**, Protein (Escherichia coli clone pHAP1 gene envM reduced)
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); PROC (Process)
(amino acid sequence; **enoyl**-ACP (**acyl carrier protein**) **reductase**-interacting substances in antimicrobial screening)

RN 148998-18-9 HCAPLUS

CN Protein (Escherichia coli clone pHAP1 gene envM reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT **37251-08-4, Enoyl-ACP reductase**
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(**enoyl-ACP (acyl carrier protein) reductase**-interacting substances in antimicrobial screening)

RN 37251-08-4 HCAPLUS
CN Reductase, enoyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L67 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:359660 HCAPLUS
DN 131:28638
ED Entered STN: 11 Jun 1999
TI Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection
IN Griffais, Remy
PA Genset, Fr.
SO PCT Int. Appl., 1912 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N015-31
ICS C12N015-62; C07K014-295; C07K016-12; C07K019-00; A01K067-027; A61K039-118; G01N033-53; C12Q001-68
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 10, 63
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9927105	A2	19990603	WO 1998-IB1890	19981120	<--
	WO 9927105	A3	19991111			
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	CA 2307846	AA	19990603	CA 1998-2307846	19981120	<--
	AU 9911702	A1	19990615	AU 1999-11702	19981120	<--
	AU 762606	B2	20030626			
	EP 1032674	A2	20000906	EP 1998-954662	19981120	<--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI					
	BR 9814878	A	20001003	BR 1998-14878	19981120	<--
	JP 2002536958	T2	20021105	JP 2000-556579	19981120	<--
	US 6559294	B1	20030506	US 1998-198452	19981123	<--
	US 2004006218	A1	20040108	US 2002-289762	20021107	<--
PRAI	FR 1997-14673	A	19971121	<--		
	US 1998-107078P	P	19981104	<--		
	WO 1998-IB1890	W	19981120	<--		
	US 1998-198452	A3	19981123	<--		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES	
WO 9927105	ICM	C12N015-31	
	ICS	C12N015-62; C07K014-295; C07K016-12; C07K019-00; A01K067-027; A61K039-118; G01N033-53; C12Q001-68	
WO 9927105	ECLA	C07K014/295	<--
US 6559294	ECLA	C07K014/295	<--
US 2004006218	ECLA	C07K014/295	<--

AB The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of Chlamydia pneumoniae, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The complete genome sequence of C. pneumoniae strain CM1 (ATCC 1260-VR) is

provided, as well as 1296 open reading frames and the deduced amino acid sequences of their protein products. The invention also relates to transcriptional gene products of the Chlamydia pneumoniae genome, such as, for example, antisense and ribozyme mols., which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing Chlamydia pneumoniae infection. The invention also relates to a method of selecting compds. capable of modulating bacterial infection and a method for the biosynthesis or biodegrdn. of mols. of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compns. for the prevention and/or treatment of bacterial, in particular Chlamydia pneumoniae, infections.

ST Chlamydia pneumoniae genome sequence; open reading frame sequence Chlamydia pneumoniae; protein sequence Chlamydia pneumoniae; infection diagnosis treatment Chlamydia pneumoniae genome

IT Antibacterial agents
Chlamydia pneumoniae
DNA sequences
Drug screening
Genome
Immunization
Immunoassay
Nucleic acid amplification (method)
Nucleic acid hybridization
Protein sequences
Test kits
Vaccines
(Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Antibodies
Primers (nucleic acid)
Probes (nucleic acid)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Gene, microbial
Lipoproteins
Proteins, general, biological studies
Transport proteins
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Antigens
Fusion proteins (chimeric proteins)
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(KDO-related; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(RGD-containing; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Infection
(bacterial; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP

(Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(lipid A component-related; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Carbohydrates, biological studies
Proteins, general, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism, proteins involved in; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Diagnosis
(mol.; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Gene
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(open reading frame; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(phosphoglucomutase-related; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(phosphomannomutase-related; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Cell envelope
(proteins in; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Amino acids, biological studies
Fatty acids, biological studies
Nucleic acids
Nucleotides, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proteins involved in metabolism of; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Cell wall
(proteins involved in synthesis of; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Lipopolysaccharides
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proteins involved in synthesis of; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Development, microbial
Secretion (process)
Transcription, genetic
Translation, genetic
Virulence (microbial)
(proteins involved in; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Molecular cloning
(recombinant expression systems; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(surface-exposed; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention

and treatment of infection)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(transmembrane; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT 172279-76-4 223700-82-1 223701-03-9 223701-17-5 223701-43-7
223701-52-8 223701-59-5 223701-74-4 223701-77-7 **223701-95-9**
223701-98-2 223702-01-0, Protein (Chlamydia pneumoniae gene ycfF) 223702-14-5 223702-35-0 **223702-38-3** 223702-42-9
223702-49-6 223702-53-2 223702-64-5 223702-65-6 223702-66-7
223702-75-8 223702-79-2 223702-84-9, Protein (Chlamydia pneumoniae gene kpsF) 223702-87-2 223703-03-5 223703-08-0 223703-11-5
223703-17-1 223703-21-7 223703-28-4 223703-30-8 223703-34-2
223703-76-2 223703-77-3 223703-81-9 223703-93-3 223703-95-5
223703-98-8 223704-09-4 223704-13-0 223704-15-2 223704-21-0
223704-24-3 223704-27-6 223704-44-7 223704-64-1 223704-79-8
223704-80-1 223704-83-4 223704-87-8, Protein (Chlamydia pneumoniae gene gidA) 223704-90-3 223704-91-4 223705-27-9 223705-30-4
223705-31-5 223705-36-0 223705-37-1 223705-39-3 223705-46-2
223705-53-1 **223705-54-2** 223705-58-6 223705-63-3
223705-65-5 223706-11-4 223706-23-8 223706-27-2 223706-33-0
223706-45-4 223706-46-5 223706-48-7 223706-53-4 223706-59-0, Protein (Chlamydia pneumoniae gene yscN) 223706-63-6 223706-76-1
223706-79-4 223706-81-8 223706-89-6 223707-24-2 223707-33-3
223707-35-5 223707-52-6 223707-77-5 223708-11-0 223708-21-2
223708-41-6 223708-42-7 223708-44-9 223708-80-3 223708-86-9
223709-35-1 223709-48-6 223709-49-7 223709-61-3 223710-10-9
223710-18-7 223710-19-8 223710-25-6 223710-42-7 223711-54-4
223711-89-5 223711-98-6 223712-07-0 223712-08-1 223712-09-2
223712-18-3 223712-20-7 223712-26-3 223712-47-8 223712-93-4
223712-98-9 223712-99-0 223713-13-1 223713-15-3, Protein (Chlamydia pneumoniae gene gp6D) 223713-16-4 223713-23-3 223713-24-4
223713-26-6 223713-52-8, Protein (Chlamydia pneumoniae gene mreB)
223713-57-3 223713-58-4 223713-59-5 223713-63-1 223713-65-3
223713-75-5 223713-82-4 223714-56-5, Protein (Chlamydia pneumoniae gene yycJ) 223714-71-4 223714-77-0 223714-85-0 223714-91-8
223714-95-2 223715-04-6 223715-15-9 223715-93-3 223715-95-5
223715-96-6 223715-97-7 223715-98-8, Protein (Chlamydia pneumoniae gene cysQ) 223716-13-0 223716-56-1 223716-61-8 223716-65-2
223716-68-5 223716-71-0 223717-27-9 223717-36-0 223717-37-1
223717-41-7, Protein (Chlamydia pneumoniae gene mesJ) 223717-57-5
223717-79-1 223717-93-9 223718-04-5 223718-43-2 223718-46-5
223718-50-1 223718-68-1, Protein (Chlamydia pneumoniae gene yfgA)
223718-75-0 223718-85-2 223718-87-4 223718-91-0 223718-92-1
223718-93-2 223740-15-6 223741-15-9 225923-41-1 225923-42-2
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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT 226079-04-5 226079-05-6 226079-06-7 226079-07-8 226079-08-9

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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT 226388-41-6 226388-42-7 226388-43-8 226388-44-9 226388-45-0
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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT 226402-35-3 226402-36-4 226402-37-5 226402-38-6 226402-39-7
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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT 226408-00-0 226408-01-1 226408-02-2 226408-03-3 226408-04-4
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RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

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226555-59-5 226555-60-8 226555-61-9 226555-63-1 226555-64-2
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226556-35-0 226556-36-1 226556-37-2 226556-38-3 226556-39-4
226556-40-7 226556-41-8 226556-42-9 226556-43-0 226556-44-1
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226556-50-9 226556-51-0 226556-52-1 226556-53-2 226556-54-3
226556-55-4 226556-56-5 226556-57-6 226556-58-7
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT 226556-59-8 226556-61-2 226556-62-3 226556-63-4 226556-64-5
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226556-70-3 226556-71-4 226556-72-5 226556-74-7 226556-75-8
226556-76-9 226556-77-0 226556-78-1 226556-80-5 226556-81-6
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226556-92-9 226556-93-0 226556-94-1 226556-95-2 226556-96-3
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226557-02-4 226557-03-5 226557-04-6 226557-05-7 226557-06-8
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226557-14-8 226557-15-9 226557-16-0 226557-17-1 226557-18-2
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226557-39-7 226557-40-0 226557-41-1 226557-42-2 226557-43-3
226557-44-4 226557-45-5 226557-46-6 226557-47-7 226557-48-8
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226557-69-3 226557-70-6 226557-71-7 226557-72-8 226557-73-9
226557-74-0 226557-75-1 226557-76-2 226557-77-3 226558-75-4
226565-57-7 226565-58-8 226700-83-0 226711-74-6 226711-75-7
226711-76-8 226711-77-9 226711-78-0 226711-79-1 226711-81-5
226711-82-6 226711-83-7 226711-84-8 226711-85-9 226711-86-0
226711-89-3 226711-90-6 226711-91-7 226711-92-8 226711-93-9
226711-94-0 226890-64-8 226918-15-6 226918-16-7 226918-17-8
226918-18-9 226918-19-0
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)

IT **223701-95-9 223701-98-2 223702-38-3**
223705-53-1 223705-54-2
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Chlamydia pneumoniae genomic sequence and polypeptides and their fragments and uses for the diagnosis, prevention and treatment of infection)
RN 223701-95-9 HCAPLUS
CN Acyl carrier protein (Chlamydia pneumoniae gene acpP) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 223701-98-2 HCAPLUS
CN Acyl carrier protein (Chlamydia pneumoniae gene fabD) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 223702-38-3 HCAPLUS
CN Acyltransferase, [acyl carrier protein] (Chlamydia pneumoniae gene acpS) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 223705-53-1 HCAPLUS
CN Acyltransferase, uridine diphosphoacetylglucosamine (Chlamydia pneumoniae gene lpxA) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 223705-54-2 HCAPLUS
CN Dehydratase, D-3-hydroxypalmitoyl-[acyl carrier protein] (Chlamydia pneumoniae gene fabZ) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L67 ANSWER 6 OF 6 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:627781 HCAPLUS
DN 117:227781
ED Entered STN: 13 Dec 1992
TI DNA sequence comprising at least part of a gene for stearoyl-ACP desaturase, and its use in altering fatty acid biosynthesis in plants
PA Stichting voor de Technische Wetenschappen te Utrecht, Neth.
SO Neth. Appl., 31 pp.
CODEN: NAXXAN
DT Patent
LA Dutch
IC ICM C12N015-53
ICS A01H005-00; A23D009-02
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 11, 17
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI NL 9002130	A	19920416	NL 1990-2130	19900928 <--
PRAI NL 1990-2130		19900928 <--		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
NL 9002130	ICM	C12N015-53
	ICS	A01H005-00; A23D009-02

AB Fatty acid biosynthesis is altered in a temperate-zone plant to provide an oil having more desirable properties, e.g. a higher saturated fatty acid content, by introduction into the plant of a DNA expression cassette containing at least part of a gene for stearoyl acyl carrier protein (ACP) .DELTA.9-desaturase (I) from a cruciferous plant. The cassette may include a promoter which is either constitutive or seed-specific (e.g. a napin or cruciferin promoter). The DNA sequence may be introduced in the antisense direction to diminish the amount of I produced by a plant already having a I gene, or in the sense direction to evoke or enhance I production Thus, a cDNA library from Brassica napus embryos was constructed and screened with antibodies to I, and the I-encoding DNA was sequenced and ligated to a napin promoter and a chalcone synthase trailer sequence to provide seed-specific expression cassette pAR4. A cocoa butter equivalent is obtained from plants such as B. napus transformed with the cassette.
ST stearoyl ACP desaturase Brassica cDNA cloning; sequence stearoyl ACP desaturase Brassica cDNA; fatty acid biosynthesis transgenic plant; cocoa butter substitute transgenic Brassica

IT Gene, plant
RL: BIOL (Biological study)
(for stearoyl acyl carrier protein desaturase gene, plant transformation with, fatty acid formation in relation to)
IT Cocoa butter substitutes
(formation of, by plant transformed with stearoyl acyl carrier protein desaturase gene)
IT **Fatty acids, biological studies**
RL: FORM (Formation, nonpreparative)
(formation of, by plant, transformation with expression cassette containing stearoyl acyl carrier protein desaturase gene effect on)
IT Deoxyribonucleic acid sequences
(of stearoyl acyl carrier protein desaturase cDNA of Brassica napus)
IT Molecular cloning
(of stearoyl acyl carrier protein desaturase gene of Brassica napus)
IT Protein sequences
(of stearoyl acyl carrier protein desaturase of Brassica napus)
IT Plasmid and Episome
(pAR14, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)
IT Plasmid and Episome
(pAR20, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)
IT Plasmid and Episome
(pAR23, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)
IT Plasmid and Episome
(pAR24, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)
IT Plasmid and Episome
(pAR31, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)
IT Plasmid and Episome
(pAR4, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)
IT Plasmid and Episome
(pDES7, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)
IT Plasmid and Episome
(pROKI, 35S promoter of cauliflower mosaic virus on, in expression cassette construction for stearoyl acyl carrier protein desaturase gene transformation into plants)
IT **Nucleic acid hybridization**
(probe, stearoyl acyl carrier protein desaturase gene fragment as)
IT Seed
(promoter specific for, expression cassette containing stearoyl acyl carrier protein desaturase gene and, plant transformation with, fatty acid formation in relation to)
IT Brassica
Brassica napus
Crucifer
(stearoyl acyl carrier protein desaturase gene of, plant transformation with, fatty acid formation in relation to)
IT Plant
(stearoyl acyl carrier protein desaturase gene transformation of, fatty acid formation in relation to)
IT Antibodies
RL: BIOL (Biological study)
(to stearoyl acyl carrier protein desaturase)
IT Virus, plant
(cauliflower mosaic, 35S promoter of, on expression cassette for stearoyl acyl carrier protein desaturase gene transformation into plants)
IT Globulins, biological studies
RL: BIOL (Biological study)
(cruciferins, gene promoter for, expression cassette containing stearoyl acyl carrier protein desaturase gene and, plant transformation with, fatty acid formation in relation to)
IT Albumins, biological studies
RL: BIOL (Biological study)
(napins, gene promoter for, expression cassette containing stearoyl acyl carrier protein desaturase gene and, plant transformation with, fatty acid formation in relation to)
IT Plasmid and Episome
(pAR10, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)

IT Plasmid and Episome
(pAR30, stearoyl acyl carrier protein desaturase gene on, plant transformation with, fatty acid formation in relation to)
IT Genetic element
RL: BIOL (Biological study)
(promoter, for cruciferin and napin genes, expression cassette containing stearoyl acyl carrier protein desaturase gene and, plant transformation with, fatty acid formation in relation to)
IT Genetic element
RL: BIOL (Biological study)
(terminator, of chalcone synthase gene, expression cassette containing stearoyl acyl carrier protein desaturase gene and, plant transformation with, fatty acid formation in relation to)
IT **144518-47-8**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete, and plant transformation with gene for, fatty acid formation in relation to)
IT **37256-86-3**
RL: BIOL (Biological study)
(gene for, plant transformation with, fatty acid formation in relation to)
IT **144518-44-5 144518-46-7**, Deoxyribonucleic acid (Brassica napus clone pAR10 1-73-[acyl carrier protein] acyldesaturase-specifying)
RL: BIOL (Biological study)
(nucleotide sequence of and plant transformation with, fatty acid formation in relation to)
IT **144518-45-6**, Deoxyribonucleic acid (Brassica napus clone pAR10 [acyl carrier protein] acyldesaturase messenger RNA-complementary)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of, complete, and plant transformation with, fatty acid formation in relation to)
IT 56803-04-4, Chalcone synthase
RL: BIOL (Biological study)
(terminator of gene for, expression cassette containing stearoyl acyl carrier protein desaturase gene and, plant transformation with, fatty acid formation in relation to)
IT **144518-47-8**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete, and plant transformation with gene for, fatty acid formation in relation to)
RN 144518-47-8 HCAPLUS
CN Desaturase, acyl- [acyl carrier protein] (Brassica napus clone pAR10 precursor reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **37256-86-3**
RL: BIOL (Biological study)
(gene for, plant transformation with, fatty acid formation in relation to)
RN 37256-86-3 HCAPLUS
CN Desaturase, acyl-[acyl carrier protein] (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **144518-44-5 144518-46-7**, Deoxyribonucleic acid (Brassica napus clone pAR10 1-73-[acyl carrier protein] acyldesaturase-specifying)
RL: BIOL (Biological study)
(nucleotide sequence of and plant transformation with, fatty acid formation in relation to)
RN 144518-44-5 HCAPLUS
CN DNA, (Brassica napus clone pAR10 [acyl carrier protein] acyldesaturase cDNA plus flanks) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 144518-46-7 HCAPLUS
CN DNA (Brassica napus clone pAR10 1-73-[acyl carrier protein] acyldesaturase-specifying) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **144518-45-6**, Deoxyribonucleic acid (Brassica napus clone pAR10 [acyl carrier protein] acyldesaturase messenger RNA-complementary)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of, complete, and plant transformation with, fatty acid formation in relation to)
RN 144518-45-6 HCAPLUS

CN DNA (Brassica napus clone pAR10 [acyl carrier protein] acyldesaturase cDNA) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

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FILE 'HOME' ENTERED AT 15:24:23 ON 09 SEP 2004

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